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(54) Title: TGF-β TYPE RECEPTOR cDNAS AND USES THEREFOR

#### (57) Abstract

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DNA encoding TGF- $\beta$  type III receptor of mammalian origin, DNA encoding TGF- $\beta$  type II receptor of mammalian origin, TGF- $\beta$  type III receptor, TGF- $\beta$  type III receptor and uses therefor.

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-1-

#### TGF-8 TYPE RECEPTOR CDNAs AND USES THEREFOR

#### Description

#### Background

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Transforming growth factor-beta (TGF- $\beta$ ) is a member 5 of a family of structurally related cytokines that elicit a variety of responses, including growth, differentiation, and morphogenesis, in many different cell types. (Roberts, A.B. and M.B. Sporn, In: Peptide Growth Factors and Their Receptors, Springer-Verlag, Heidelberg, 10 pp. 421-472 (1990); Massague, J., Annu. Rev. Cell. Biol. 6:597-641 (1990)) In vertebrates at least five different forms of TGF- $\beta$ , termed TGF- $\beta$ 1 to TGF- $\beta$ 5, have been identified; they all share a high degree (60%-80%) of amino-acid sequence identity. While  $TGF-\beta 1$  was initially 15 characterized by its ability to induce anchorageindependent growth of normal rat kidney cells, its effects on most cell types are anti-mitogenic. (Altschul, S.F. et al., J. Mol. Biol. 215:403-410 (1990); Andres, J.L. et al., J. Cell. Biol. 109:3137-3145 (1989)). It is 20 strongly growth-inhibitory for many types of cells, -- including both normal and transformed epithelial, endothelial, fibroblast, neuronal, lymphoid, and hematopoietic cells. In addition,  $TGF-\beta$  plays a central role in regulating the formation of extracellular matrix and 25 cell-matrix adhesion processes.

In spite of its widespread effects on cell phenotype and physiology, little is known about the biochemical mechanisms that enable  $TGF-\beta$  family members to elicit these varied responses. Three distinct high-affinity

cell-surface TGF-β-binding proteins, termed type I, II and III, have been identified by incubating cells with radiolabelled TGF-β1, cross-linking bound TGF-β1 to cell surface molecules, and analyzing the labelled complexes by polyacrylamide gel electrophoresis. (Massague, J. and B. Like, J. Biol. Chem. 260:2636-2645 (1985); Cheifetz, S. et al. J. Biol. Chem. 261:9972-9978 (1986).) The binding constants are about 5-50pM for the type I and II receptor and 30-300 pM for the type III receptor. (Boyd, F.T. and J. Massague, J. Biol. Chem. 264:2272-2278

The type I and II receptors, of estimated 53 and 70-100 kilodaltons mass respectively, are N-glycosylated transmembrane proteins that are similar in many respects. Each of these receptors has a distinct affinity for each 15 member of the TGF- $\beta$  family of ligands. (Boyd, F.T. and J. Massague, J. Biol. Chem. 264:2272-2278 (1989)) contrast, the type III receptor shows comparable affinities for all TGF- $\beta$  isotypes; the type III receptor is the most abundant cell-surface receptor for TGF-\$\beta\$ in many 20 cell lines (upwards of 200,000 per cell), and is an integral membrane proteoglycan. It is heavily modified by glycosaminoglycan (GAG) groups, and migrates heterogeneously upon gel electrophoresis as proteins of 280 to 330 kilodaltons. When deglycosylated with heparitinase 25 and chondrontinase, the protein core migrates as a 100-110 kilodalton protein. The TGF- $\beta$  binding site resides in this protein core, as non-glycosylated forms of this receptor that are produced in cell mutants defective in GAG synthesis are capable of ligand binding 30 with affinities comparable to those of the natural receptor. (Cheifetz, S. and J. Massague, J. Biol. Chem., 264:12025-12028 (1989) A variant form of type III

receptor is secreted by some types of cells as a soluble molecule that apparently lacks a membrane anchor. This soluble species is found in low amounts in serum and in extracellular matrix.

The type III receptor, also called betaglycan, has a 5 biological function distinct from that of the type I and II receptors. Some mutant mink lung epithelial cell (Mv1Lu) selected for loss of TGF- $\beta$  responsiveness no longer express type I receptors; others, similarly selected, lose expression of both the type I and II 10 receptors. However, all these variants continue to express the type III receptor. (Boyd, F.T. and J. Massague, J. Biol. Chem. 264:2272-2278 (1989); Laiho, M. et al., J. Biol. Chem. 265:18518-18524 (1990)) This has led to the proposal that types I and II receptors are 15 signal-transducing molecules while the type III receptor, may subserve some other function, such as in concentrating ligand before presentation to the bona fide signal-transducing receptors. The secreted form of type III receptor, on the other hand, may act as a reservoir 20 or clearance system for bioactive TGF- $\beta$ .

Additional information about each of these  $TGF-\beta$  receptor types would enhance our understanding of their roles and make it possible, if desired, to alter their functions.

#### 25 Summary of the Invention

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The present invention relates to isolation, sequencing and characterization of DNA encoding the TGF- $\beta$  type III receptor of mammalian origin and DNA encoding the TGF- $\beta$  type II receptor of mammalian origin. It also relates to the encoded TGF- $\beta$  type III and type II receptors, as well as to the soluble form of each; uses

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of the receptor-encoding genes and of the receptors themselves; antibodies specific for TGF-β type III receptor
and antibodies specific for TGF-β type II receptor. In
particular, it relates to DNA encoding the TGF-β type III
receptor of rat and human origin, DNA encoding the TGF-β
type II receptor of human origin and homologues of each.

The TGF- $\beta$  receptor-encoding DNA of the present invention can be used to identify equivalent TGF- $\beta$ receptor type III and type II genes from other sources, using, for example, known hybridization-based methods or 10 the polymerase chain reaction. The type III receptor gene, the type II receptor gene or their respective encoded products can be used to alter the effects of TGF- $\beta$  (e.g., by altering receptivity of cells to TGF- $\beta$  or interfering with binding of  $TGF-\beta$  to its receptor), such 15 as its effects on cell proliferation or growth, cell adhesion and cell phenotype. For example, the TGF- $\beta$ receptor type III gene, the TGF- $\beta$  receptor type II gene, or a truncated gene which encodes less than the entire receptor (e.g., soluble TGF- $\beta$  type III receptor, soluble 20 TGF- $\beta$  type II receptor or the TGF- $\beta$  type III or type II binding site) can be administered to an individual in whom TGF- $\beta$  effects are to be altered. Alternatively, the TGF- $\beta$  type III receptor, the TGF- $\beta$  type II receptor, a soluble form thereof (i.e., a form lacking the membrane 25 anchor) or an active binding site of the TGF-β type III or the type II receptor can be administered to an individual to alter the effects of TGF- $\beta$ .

Because of the many roles TGF- $\beta$  has in the body, availability of the TGF- $\beta$  receptors described herein 30 makes it possible to further assess TGF- $\beta$  function utilizing in vivo as well as in vitro methods and to alter (enhance or diminish) its effects.

#### Brief Description of the Drawings

Figure 1 is the DNA sequence (SEQ ID NO. 1) and the translated amino acid sequence (SEQ ID NO. 2) of type III TGF-81 receptor cDNA clone R3-OFF (full insert size 6 kb), in which the open reading frame with flanking 5 sequences of the clone are shown. The transmembrane domain is indicated by a single underline. Peptide sequences from purified type III receptor, mentioned in text, that correspond to the derived sequence, are in italics and underlined. Potential N-linked glycosylation 10 sites are indicated by #, and extracellular cysteines by &. A consensus protein kinase C phosphorylation site is indicated by \$. The last non-vector encoded amino acid of Clone R3-OF (2.9 kb) is indicated by @. Consensus proteoglycan attachment site is indicated by +++. 15 potential glycosaminoglycan attachment sites are indicated by +. The upstream in-frame stop codon (-42 to -44) is indicated by a wavy line. Signal peptide cleavage site predicted by vonHeijne's algorithm (von Heijne, G., Nucl. Acid. Res. 14:4683-4690 (1986) is 20 indicated by an arrow.

Figure 2 is the nucleotide sequence of the fulllength type II TGF-β receptor cDNA clone 3FF isolated from a human HepG2 cell cDNA library (full insert size 5 kb) (SEQ ID NO. 3). The cDNA has an open reading frame 25 encoding a 572 amino acid residue protein.

Figure 3 is the amino acid sequence of the fulllength type II TGF- $\beta$  receptor (SEQ ID NO. 4).

#### Detailed Description of the Invention

The subject invention is based on the isolation and 30 sequencing of DNA of vertebrate, particularly mammalian, origin which encodes TGF-β type III receptor and DNA of mammalian origin which encodes TGF-β type II receptor,

expression of the encoded products and characterization of the expressed products. As described, a full-length cDNA which encodes TGF-β receptor type III has been isolated from a cDNA library constructed from a rat vascular smooth muscle cell line and a full-length cDNA which encodes TGF-β type II receptor has been isolated from a human cDNA library. The human homologue of the type III gene has also been cloned. A deposit of human TGF-β type III cDNA in the plasmid pBSK has been made under the terms of the Budapest Treaty at the American Type Culture Collection (10/21/91) under Accession Number 75127. All restrictions upon the availability of the deposited material will be irrevocably removed upon granting of a U.S. patent based on the subject

# Isolation and Characterization of TGF-\$ Type III Receptor

As described herein, two separate strategies were pursued for the isolation of the TGF- $\beta$  type III receptor 20 cDNA. In one approach, monoclonal antibodies were generated against the type III receptor protein and used to purify the receptor, which was then subjected to microsequencing. (See Example 1) Microsequencing of several peptides resulting from partial proteolysis of 25 the purified receptor produced four oligopeptide sequences, which were used to construct degenerate oligonucleotides. The degenerate oligonucleotides were used either as primers in a cloning strategy using the polymerase chain reaction (PCR) or as probes in screening 30 cDNA libraries. Although this strategy did not prove to be productive, the oligopeptide sequences were useful in verifying the identity of the receptor clones isolated by the second strategy.

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In the second approach to isolating TGP-β receptorencoding clones, an expression cloning strategy was used in COS cells; direct visualization of receptor positive cells was used to isolate receptor cDNAs. (See Example In this approach, a cDNA library was constructed from A-10 cells, a rat vascular smooth muscle cell line which expresses all three TGF- $\beta$  receptors (type I, II and III). COS cells transfected with cDNA components of this library in a vector carrying the cytomegalovirus (CMV) transcriptional promoter and the SV40 origin of repli-10 cation were screened to identify cells expressing substantially higher than normal levels of TGF- $\beta$  receptor. One transfectant expressing such high levels of a TGF- $\beta$ binding protein was identified and the original pool of expression constructs from which it was derived was split 15 into subpools, which were subjected to a second round of screening. Two further rounds of sib-selection resulted in isolation of one cDNA clone (R3-OF) with a 2.9 kb insert which induced high levels of TGF-\$-binding proteins in approximately 10% of cells into which it was 20 introduced. The specificity of the TGF- $\beta$  binding was validated by showing that addition of a 200-fold excess unlabeled competitor TGF- $\beta$ 1 strongly reduced binding of 125 I-TGF- $\beta$  to transfected cells.

The R3-OF cDNA encoded an open reading frame of 817 25 amino acid residues, but did not contain a stop codon. R3-OF was used as a probe to isolate a full-length cDNA from a rat 208F library. The resulting clone, R3-OFF, is 6kb in length and encodes a protein of 853 amino acids, which is colinear with clone R3-OF. The nucleotide 30 sequence of R3-OFF is shown in Figure 1, along with the translated amino acid sequence.

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Characterization of the receptor encoded by R3-OFF was carried out, as described in Example 3. Results . showed three distinct TGF- $\beta$  binding protein species of TGF- $\beta$  on the surface of mock-transfected COS cells, which is in accord with results reported by others. (Massague, J. et al., Ann. NY Acad. Sci. 593:59-72 (1990)). included the two lower molecular weight type I and II receptors (65 and 85 kD) and the higher molecular weight type III proteoglycan, which migrates as a diffuse band of 280-330 kd. Enzymatic removal of the proteoglycan 10 yielded a core protein of approximately 100 kd. Binding to all three receptor types is specific in that it was competed by 200-fold excess of unlabeled TGF-\$1.

Transfecting the isolated cDNA caused a two-fold increase in expression of the type III receptor. When a cell lysate derived from COS cells transfected with clone R3-OFF was treated with deglycosylating enzymes, the heterogeneous 280-330 kd band was converted to a protein core which co-migrates with the type III protein core seen in parental A10 cells. Importantly, the recombinant protein core migrated differently from the endogenous COS cell type III protein core.

These observations were confirmed and extended using stably transfected cells expressing the type III cDNA. L6 rat skeleton muscle myoblasts do not express any 25 detectable type III mRNA and no endogeneous surface type III receptor (Massague et al., 1986; Segarini et al., 1989). These cells were transfected with the isolated cDNA in the vector pcDNA-neo. Cell clones stably expressing this clone in both the forward and reverse orientations with respect to the CMV promoter were isolated and analyzed by ligand binding assay.

Introduction of either the full-length clone R3-OFF or the partial clone R3-OF in the forward orientation resulted in expression of type III receptor. L6 cells transfected with the cDNA clones in the reverse orientation did not express this protein. Importantly, the apparent size of the protein core of the type III receptor in cells transformed with the R3-OF clone is smaller than that from R3-OFF transformed cells, consistent with the difference in the sizes of the protein cores predicted from their nucleic acid sequences.

Surprisingly, binding of radio-labeled ligand to the type II receptor was increased by 2.5 fold in cells expressing the type III cDNA. Binding to the type I receptor was unchanged. This apparently specific up-regulation of ligand-binding to the type II receptor was evident in all of the 15 stably transfected L6 cell lines analyzed to date. Furthermore, this effect seems to be mediated equally well by the full-length clone or a truncated clone (R3-OF) that lacks the cytoplasmic domain of TGF-β type III receptor was expressed.

Expression of type III receptor mRNA was assessed by Northern blot analysis and RNA blot analysis. Northern gel analysis showed that the type III receptor mRNA is expressed as a single 6 kb message in several rat

25 tissues. RNA dot blot analysis of several different tissue culture cell lines was also carried out. Cells of mouse origin (MEL and YH16) appear to express a smaller (~5.5 kb) message for the type III mRNA than those of pig, rat and human origin. In all of these cells,

30 expression or absence of the type III mRNA is consistent with the expression or absence of detectable cell surface

type III receptors, with the notable exception of the retinoblastoma cell lines (Y79, Weri-1, Weri-24, and Weri-27). These cells lack detectable surface expression of type III receptor, which confirms an earlier report. (Kimchi, A. et al., Science 240:196-198 (1988)). It is striking that the type III receptor mRNA is expressed in these cells at a level comparable to that of other cells that do indeed express type III receptor proteins at readily detectable levels. It appears that  $TGF-\beta$  receptor III expression, which is substantial in normal retinoblasts (AD12), has been down-regulated in these retinoblastoma tumor cells, perhaps through post-transcriptional mechanisms.

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The nucleotide sequence full reading frame along with flanking sequences of the full-length cDNA clone 15 R3-OFF was determined and is presented in Figure 1. The reading frame encodes a protein of 853 amino acid residues, which is compatible with the 100 kD size observed for the fully deglycosylated TGF-\$1 type III receptor. The identity of the receptor as  $TGF-\beta$  type III 20 was verified by searching for segments of the putative transcription product which included the peptide sequences determined by microsequencing of the isolated type III receptor. (See Example 1) As indicated in Figure 1, two segments of derived protein (underlined and 25 italicized, residues 378-388 and 427-434) precisely match with the amino acid sequences of two peptides (I and III) determined from direct biochemical analysis of the purified type III receptor.

Further analysis showed that TGF-β type III binding 30 protein has an unusual structure for a cytokine receptor. Hydropathy analysis indicates that the protein includes a

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N-terminal signal sequence, followed by a long, hydrophilic N-terminal region. A 27 residue region of strong hydrophobicity (underlined in Figure 1, residues 786-812) toward the C-terminus represents the single putative transmembrane domain. This suggests that nearly all of the receptor which is an N-terminal extracellular domain is anchored to the plasma membrane near its C-terminus. A relatively small C-terminal tail of 41 residues represents the cytoplasmic domain.

Analysis of related sequences provides few clues to 10 function of TGF-β type III protein. Only one other gene described to date, a glycoprotein expressed in high quantities by endothelial cells and termed endoglin, contains a related amino acid sequence. The most homologous regions between the sequences of the type III 15 receptor and endoglin (74%) falls primarily in the putative transmembrane and cytoplasmic domains. Similar to the general structure of type III receptor, endoglin is a glycoprotein which contains a large hydrophilic N-terminal domain which is presumably extracellular, 20 followed by a putative transmembrane domain and a short cytoplasmic tail of 47 amino acid residues. The biological role of endoglin is still unclear at present, although it has been suggested that it may involved in cell-cell recognition through interactions of an "RGD" 25 sequence on its ectodomain with other adhesion molecules. Unlike the TGF-\$\beta\$ type III receptor, endoglin does not carry GAG groups.

## Isolation of TGF-β Type II Receptor

The cDNA encoding the type II TGF-β receptor was also isolated, using expression cloning in COS cells. A full-length cDNA (designated clone 3FF) was isolated by high stringency hybridization from a human HepG2 cell cDNA library. (See Example 6) Analysis showed that the corresponding message is a 5 kb message which is expressed in different cell lines and tissues. Sequence analysis indicated that the cDNA has an open reading frame encoding a core 572 amino acid residue protein.

The nucleotide sequence of the full-length type II TGF-β receptor cDNA clone 3FF is shown in Figure 2; the amino acid sequence is represented in Figure 3.

The 572 amino acid residue protein has a single putative transmembrane domain, several consensus glycosylation sites, and a putative intracellular serine/ threonine kinase domain. The predicted size of the encoded protein core is -60 kd, which is too large for a type I TGF-β receptor. Instead, crosslinking experiments using iodinated TGF-β and COS cells transiently transfected with clone 3FF shows over-expression of a protein approximately 70-80 kd which corresponds to the size of type II TGF-β receptors. Thus, clone 3FF encodes a protein that specifically binds TGF-β and has an expressed protein size of 70-80 kd, both characteristic of the type II TGF-β receptor.

# Uses of the Cloned TGF-β Receptors and Related Products

For the first time, as a result of the work described herein, DNAs encoding two of the three high affinity cell-surface TGF-β receptors have been isolated, their sequences and expression patterns determined and

the encoded proteins characterized. Expression of the  $TGF-\beta$  type III receptor in cells which do not normally express the receptor, followed by ligand binding assay, verified that the cloned type III receptor-encoding DNA (i.e., either the full-length clone R3-OFF or the partial clone R3-OF) encoded the receptor. In addition, the work described herein resulted in the surprising finding that binding of  $TGF-\beta$  to type II receptors in cells expressing the type III DNA was increased by 2.5 fold.

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Additional insight into the role of the TGF- $\beta$  type 10 III receptor and its interaction with TGF-β type II receptor is a result of the work described. For example, the role of TGF- $\beta$  type III receptor is unclear, but it has been proposed that it serves a most unusual function of attracting and concentrating TGF- $\beta$ s for eventual 15 transfer to closely situated signal-transducing receptors. While most cytokines bind to a single cell surface receptor, members of the TGF-\$\beta\$ family bind with greater or lesser affinity to three distinct cell surface proteins. This has raised the question of why these 20 three receptors are displayed by most cell types and whether they subserve distinct functions. Evidence obtained to date suggests that the type III receptor may perform functions quite different from those of types I and II. Thus, type III is substantially modified by GAGs 25 while types I and II appear to carry primarily the N-linked (and perhaps O-linked) sidechains that are characteristic of most growth factor receptors. In addition, variant cells that have been selected for their ability to resist TGF- $\beta$ -induced growth inhibition show 30 the absence of Type I or Type II receptors while continuing to display Type III receptors. Together, these data have caused some to propose that the Type I

PCT/US92/09326 WO 93/09228

and II receptors represent bona fide signal-transducing receptors while the type III receptor, described here, plays another distinct role in the cell.

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It remains possible that the type III receptor serves a most unusual function of attracting and concentrating TGF- $\beta$ s on the cell surface for eventual transfer to closely situated signal-transducing receptors. Such a function would be unprecedented for a proteinaceous receptor, although heparin sulfate has been shown to activate basic FGF by binding to this growth 10 factor prior to FGF association with its receptor (Yayon, A. et al., Cell 64:841-848 (1991)) Parenthetically, since the type III receptor also contains large quantities of heparan sulfate side-chains, it may also bind and present basic FGF to its receptor.

Evidence that is consistent with the role for the type III receptor comes from the work with L6 rat myoblast cells which is described herein. As described above, in L6 cells overexpressing type III receptor, the binding of radiolabelled TGF- $\beta$  to the type II receptor is increased several fold when compared with that seen with parental cells. Further assessment of TGF- $\beta$  type III function and interaction with type II and type I receptors will be needed to answer these questions and can be carried out using the materials and methods described here.

TGF- $\beta$  receptors, both type III and type II, can be identified in other species, using all or a portion of the DNA encoding the receptor to be identified as a probe and methods described herein. For example, all or a portion of the DNA sequence encoding TGF- $\beta$  type III receptor (shown in Figure 1) or all or a portion of the

DNA sequence encoding TGF- $\beta$  type II receptor (shown in Figure 2) can be used to identify equivalent sequences in other animals. Stringency conditions used can be varied, as needed, to identify equivalent sequences in other species. Once a putative TGF-β receptor type III or type 5 II-encoding sequence has been identified, whether it encodes the respective receptor type can be determined using known methods, such as described herein for verification that the cDNA insert of full-length clone R3-OFF and the cDNA insert of partial clone R3-OF encode 10 the type III receptor. For example, DNA isolated in this manner can be expressed in an appropriate host cell which does not express the receptor mRNA or the surface receptor (e.g., L6 rat skeleton muscle myoblasts) and analyzed by ligand binding (TGF- $\beta$  binding) assay, as 15 described herein.

Also as a result of the work described herein, antibodies (polyclonal or monoclonal) specific for the cloned TGF- $\beta$  type III or the clones TGF- $\beta$  type II receptor can be produced, using known methods. Such 20 antibodies and host cells (e.g., hybridoma cells) producing the antibodies are also the subject of the present invention. Antibodies specific for the cloned TGF- $\beta$  receptor can be used to identify host cells expressing isolated DNA thought to encode a TGF-\$ 25 receptor. In addition, antibodies can be used to block or inhibit  $TGF-\beta$  activity. For example, antibodies specific for the cloned TGF- $\beta$  type III receptor can be used to block binding of  $TGF-\beta$  to the receptor. They can be administered to an individual for whom reduction of 30 TGF-8 binding is desirable, such as in some fibrotic diseases (e.g., of skin, kidney and lung).

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The method of the present invention can be used for diagnosis of disorders involving abnormal binding of . TGF- $\beta$  to TGF- $\beta$  type III receptors and/or TGF- $\beta$  type II receptors, such as fibrotic diseases. Abnormal binding of TGF- $\beta$  to TGF- $\beta$  type III receptor or TGF- $\beta$  type II receptor at a cell surface may be measured, resulting in a test binding value, which is compared to an appropriate control binding value. Control binding values can be obtained using control cells known to have abnormal binding of TGF- $\beta$  to its receptors or control cells which 10 are normal cells (e.g., evidence TGF- $\beta$  binding to the TGF- $\beta$  receptor is within physiological levels). Control values are obtained by determining the extent to which TGF- $\beta$  binds the appropriate receptor (i.e., TGF- $\beta$  type III receptor or TGF- $\beta$  type II receptor); such values can 15 be obtained at the time the test binding value is determined or can be previously determined (i.e., a previously determined standard). A test binding value similar to the control binding value obtained from abnormal cells is indicative of abnormal binding of TGF-eta20 to TGF- $\beta$  type III receptor or TGF- $\beta$  type II receptor. A test binding value similar to the control binding value obtained from normal cells is indicative of normal binding of TGF- $\beta$  to TGF- $\beta$  type III receptor or TGF- $\beta$  type II receptor.

DNA and RNA encoding TGF- $\beta$  type III receptor and DNA and RNA encoding TGF- $\beta$  type II receptor are now available. As used herein, the term DNA or RNA encoding the respective TGF- $\beta$  receptor includes any oligodeoxynucleotide or oligodeoxyribonucleotide sequence 30 which, upon expression, results in production of a TGF- $\beta$ receptor having the functional characteristics of the

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TGF- $\beta$  receptor. That is, the present invention includes DNA and RNA which, upon expression in an appropriate host cell, produces a TGF-\$\beta\$ type III receptor which has an affinity for TGF- $\beta$  similar to that of the TGF- $\beta$  type III receptor on naturally occurring cell surfaces (e.g., it shows comparable affinities for all TGF- $\beta$  isotypes). Similarly, the present invention includes DNA and RNA which, upon expression in an appropriate host cell, produces a TGF- $\beta$  type II receptor which has an affinity for TGF- $\beta$  similar to that of TGF- $\beta$  type II receptor on 10 naturally occurring cell surfaces (e.g., it has a distinctive affinity for each member of the TGF- $\beta$  family of ligands similar to that of the naturally occurring TGF- $\beta$  type II receptor). The DNA or RNA can be produced in an appropriate host cell or can be produced 15 synthetically (e.g., by an amplification technique such as PCR) or chemically.

The present invention also includes the isolated TGF-β type III receptor encoded by the nucleotide sequence of full-length R3-OFF, the isolated TGF-β type 20 III receptor encoded by the nucleotide sequence of partial clone R3-OF, the isolated TGF-β type II receptor encoded by the nucleotide sequence of full-length clone 3FF and TGF-β type III and type II receptors which bind TGF-β isotypes with substantially the same affinity. The isolated TGF-β type III and type II receptors can be produced by recombinant techniques, as described herein, or can be isolated from sources in which they occur naturally or synthesized chemically. As used herein, the terms cloned TGF-β type III and cloned TGF-β type II

described herein, and TGF- $\beta$  type III and type II receptors (e.g., from other species) which exhibit . substantially the same affinity for the TGF- $\beta$  isotypes as the respective receptors.

As described previously, cells in which the cloned  $TGF-\beta$  type III receptor is expressed bind  $TGF-\beta$  in essentially the same manner as do cells on which the type III receptor occurs naturally. Further analysis of ligand interactions with the cloned TGF- $\beta$  type III receptor, based upon site-directed mutagenesis of both 10 TGF- $\beta$  and the receptor, can be carried out to identify residues important for binding. For example, DNA having the sequence of Figure 1 can be altered by adding, deleting or substituting at least one nucleotide, in order to produce a modified DNA sequence which encodes a 15 modified cloned TGF- $\beta$  type III receptor. The functional characteristics of the modified receptor (e.g., its TGF- $\beta$ -binding ability and association of the binding with effects normally resulting from binding) can be assessed, using the methods described herein. Modification of the 20 cloned TGF-β type III receptor can be carried out to produce, for example, a form of the TGF- $\beta$  type III receptor, referred to herein as soluble TGF-β receptor, which is not membrane bound and retains the ability to bind the TGF- $\beta$  isotypes with an affinity substantially 25 the same as the naturally-occurring receptor. Such a TGF- $\beta$  type III receptor could be produced, using known genetic engineering or synthetic techniques; it could include none of the transmembrane region present in the naturally-occurring TGF- $\beta$  type III receptor or only a 30 small portion of that region (i.e., small enough not to

interfere with its soluble nature). For example, it can include amino acids 1 through 785 of the TGF-β type III sequence of Figure 1 or a portion of that sequence sufficient to retain TGF-β binding ability (e.g., amino acids 24-785, which does not include the signal peptide cleavage site present in the first 23 amino acids). A soluble TGF-β type II receptor (e.g., one which does not include the transmembrane and cytoplasmic domains) can also be produced. For example, it can include amino acids 1 through 166, inclusive, of Figure 3 or a sufficient portion thereof to retain TGF-β binding ability substantially the same as that of TGF-β type II receptor.

The TGF-8 type III receptor and/or type II receptor can be used for therapeutic purposes. As described above, 15 the TGF- $\beta$  family of proteins mediate a wide variety of cellular activities, including regulation of cell growth, regulation of cell differentiation and control of cell metabolism. TGF- $\beta$  may be essential to cell function and most cells synthesize TGF- $\beta$  and have TGF- $\beta$  cell surface 20 receptors. Depending on cell type and environment, the effects of TGF- $\beta$  vary: proliferation can be stimulated or inhibited, differentiation can be induced or interrupted and cell functions can be stimulated or suppressed. TGF- $\beta$  is present from embryonic stages .25 through adult life and, thus, can affect these key processes throughout life. The similarities of a particular TGF- $\beta$  (e.g., TGF- $\beta$ 1) across species and from cell to cell are considerable. For example, the amino acid sequence of a particular  $TGF-\beta$  and the nucleotide 30 sequence of the gene which encodes it regardless of

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source, are essentially identical across species. This further suggests that  $TGF-\beta$  has a critical role in essential processes.

Specifically, TGF- $\beta$  has been shown to have antiinflammatory and immune suppression capabilities, to play an important role in bone formation (by increasing osteoblast activity), inhibit cancer cell proliferation in culture, and control proliferation of glandular cells of the prostate. As a result, it has potential therapeutic applications in altering certain immune system 10 responses (and possibly in modifying immune-mediated diseases); in treating systemic bone disease (e.g., osteoporosis) and conditions in which bone growth is to be enhanced (e.g., repair of broken bones) and in controlling growth and metastasis of cancer cells. In addition,  $TGF-\beta$  appears to play a role in determining whether some cell types undergo or do not undergo mitosis. In this respect, TGF- $\beta$  may play an important role in tissue repair. Some diseases or conditions appear to involve low production or chronic overproduction of TGF- $\beta$ . (For example, results of animal studies suggest that there is a correlation between the over production of TGF- $\beta$  and diseases characterized by fibrosis in the lung, kidney, liver or in viral mediated immune expression.)

Clearly,  $TGF-\beta$  has key roles in body processes and numerous related potential clinical or therapeutic applications in wound healing, cancer, immune therapy and bone therapy. Availability of  $TGF-\beta$  receptor genes, the encoded products and methods of using them in vitro and in vivo provides an additional ability to control or

regulate  $TGF-\beta$  activity and effect in the body. For example, the TGF- $\beta$  type II or type III receptor encoded by the type II or the type III receptor genes of the subject invention can be used, as appropriate, to alter the effects of TGF- $\beta$  (e.g., to enhance the effect of TGF- $\beta$  in the body or to inhibit or reduce (totally or partially) its effects). It is also possible to administer to an individual in whom TGF-\$\beta\$ bound to TGF-\$\beta\$ type III receptor, such as soluble TGF- $\beta$  type III receptor. The present invention provides both a TGF-\$\beta\$ agonist and a 10 TGF-β antagonist. For these purposes, DNA gene encoding the entire TGF- $\beta$  type II or type III receptor, the encoded type II or type III receptor or a soluble form of either receptor can be used. Alternatively, antibodies or other ligands designed based upon these sequences or 15 specific for them can be used for this purpose.

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Knowledge of the amino acid sequences of TGF- $\beta$  type III and type II receptors makes it possible to better understand their structure and to design compounds which interfere with binding of the receptor with TGF- $\beta$ . It 20 makes possible identification of existing compounds and design of new compounds which are type III and/or type II receptor antagonists.

Cells expressing the type III and/or type II receptors of the present invention can be used to screen 25 compounds for their ability to interfere with (block totally or partially) TGF binding to the receptors. For example, cells which do not express TGF-β type III receptor (e.g., L6 rat skeleton muscle myoblasts) but have been modified to do so by incorporation of the type 30 III cDNA in an appropriate vector can be used for this

purpose. A compound to be assessed is added, for example, to tissue culture dishes containing type III. expressing cells, along with labeled TGF- $\beta$ . As a control, the same concentration of labeled TGF- $\beta$  is added to tissue culture dishes containing the same type of cells. After sufficient time for binding of TGF- $\beta$  to the receptor to occur, binding of labeled TGF- $\beta$  to the cells is assessed, using known methods (e.g., by means of a gamma counter) and the extent to whih it occurred in the 10 presence and in the absence of the compound to be assessed is determined. Comparison of the two values show whether the test compound blocked TGF- $\beta$  binding to the receptor (i.e., less binding in the presence of the compound than in its absence is evidence that the test 15 compound has blocked binding of TGF- $\beta$  to the TGF- $\beta$  type III receptor).

Alternatively, a cell line expressing the TGF-β receptor or cells expressing microinjected TGF-β receptor RNA, can be used to assess compounds for their ability to block TGF-β binding to the receptor. In this embodiment, a compound to be assessed is added to tissue culture dishes containing the cell line cells expressing microinjected TGF-β receptor RNA, along with TGF-β. As a control, TGF-β alone is added to the same type of cells expressing microinjected endothelin receptor RNA. After sufficient time for binding of TGF-β to the receptor to occur, the extent to which binding occurred is measured, both in the presence and in the absence of the compound to be assessed. Comparison of the two values shows whether the compound blocked TGF-β binding to the receptor. The TGF-β type III and type II receptors can

-23-

also be used to identify TGF-β-like substances, to purify TGF-β and to identify TGF-β regions which are responsible for binding to the respective receptors. For example, the type III receptor can be used in an affinity-based method to identify substances which bind the receptor in a manner similar to TGF-β.

The invention will now be illustrated by the following examples, which are not intended to be limiting in any way.

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#### **EXAMPLES**

Materials and methods used in Examples 1-5 are described below.

#### <u>Materials</u>

The following is a description of materials used in the work described herein.

Recombinant human TGF-\$1 was provided by Rik Derynck of Genentech. COS-M6 cells were provided by Brian Seed of the Massachusetts General Hospital and Alejandro Aruffo of Bristol-Myers-Squibb. Heparitinase was provided by Tetsuhito Kojima and Robert Rosenberg of MIT.

LLC-PK1 cells were a gift of Dennis Ausiello of the Massachusetts General Hospital. YH-16 cell were a gift of Edward Yeh of the Massachusetts General Hospital. 3-4 cells were a gift of Eugene Kaji of the Whitehead

25 Institute for Biomedical Research. All other cell lines were purchased from ATCC and grown as specified by the supplier, except as noted.

#### Expression Cloning

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Construction of cDNA Library and Generation of Plasmid Pools

10µg polyadenylated mRNA was prepared from A10 cells by the proteinase-K/SDS method (Gonda et al., Molec. 5 Cell. Biol. 2:617-624 (1982)). Double stranded cDNA was synthesized and linkered to nonpalindromic BstX1 adaptors as described by Seed, B. and A. Aruffo, Proc. Natl. Acad. Sci. USA 84:3365-3369 (1987). Acaptored cDNA was sizefractionated on a 5 to 20% potassium acetate gradient, and inserts greater than 1 kb were ligated to the plasmid vector pcDNA-1, and electroporated in the E. coliMC1061/P3, yielding a primary library with a titer of >107 recombinants. A portion of the cDNA was plated as pools of -1x104 recombinant bacteria colonies grown on 15 cm petri dishes with Luria-broth agar containing 7.5 mg/ml tetracycline and 12.5 mg/ml ampicillin. Cells were scraped off the plates in 10 mls of Luria-broth, and glycerol stocks of pooled bacteria were stored at -70°C. The remaining bacteria was used to purify plasmid DNA using the alkaline lysis mini-prep method (Sambrook, J. et al., Molecular Cloning: A Laboratory Manual, 2d Ed. (Cold Spring Harbor, NY, Cold Spring Harbor Laboratory Press (1989)).

## COS Cell Transfections and Binding Assay

Plasmid pools (each representing ~1x10<sup>4</sup> clones) were transfected into COS-M6 (subclone of COS-7 cells) by the DEAE-dextran/chloroquine method described by Seed, B. and A. Aruffo, Proc. Natl. Acad. Sci. USA 84:3365-3369 (1987). Forty-eight hours after transfection, cells were

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incubated with 50 pM125I-TGF- $\beta$ 1 (100 to 200 Ci/mmol) for 4 hours at 4°C), autoradiographic analysis of transfected cells was performed using NT-B2 photographic emulsion (Kodak) essentially as described (Gearing, D.P. et al., EMBO J. 8:3667-3676 (1989)). After development of slides, cells were air-dried and mounted with mounting media and a glass coverslip. Slides were analyzed under an Olympus OM-T1 inverted phase-contrast microscope using a dissection trans-illuminator for darkfield illumi-10 nation.

#### Subdivision of Positive Pool

Of 86 pools screened, one pool (#13) was identified as positive and a glycerol stock of bacteria corresponding to this pool was titered and 25 pools of 1000 15 clones were generated and miniprep plasmid from these pools were transfected into COS cells as described above. Several positive pools of 1000 were identified, and one was replated as 25 plates of 100 colonies. A replica was made of this positive plate and harvested. Once a 20 positive pool was identified, individual colonies were picked from the corresponding master plate and grown overnight in 3 ml liquid culture. A 2-dimensional grid representing the 100 clones was generated and a single clone, R3-OF, was isolated.

#### Cloning of R3-OFF 25

A 208F rat fibroblast library in lambda ZAP II (Stratagene) was screened at high stringency with clone R3-OF insert, and several clones with -6kb inserts were isolated, one of which is referred to as R3-OFF.

## DNA Sequencing and Sequence Analysis

Double-stranded DNA was sequenced by the dideoxy.

chain termination method using Sequenase reagents (United States Biochemicals). Comparison of the sequence to the data bases was performed using BLAST (Altschoul, S.F. et al., J. Mol. Biol. 215:403-410 (1990)).

Iodination of TGF-β

TGF-β1 was iodinated using the chloramine-T method as described (Cheifetz, S. and J.L. Andres, <u>J. Biol.</u>

10 Chem. 263:16984-16991 (1988)).

### Chemical Cross-Linking

Transfected COS cells grown on 10 cm dishes or subconfluent L6 and A-10 cells grown on 3.5 cm dishes were incubated with  $^{125}I-TGF-\beta 1$  in binding buffer 15 (Frebs-Ringer buffered with 20 mM Hepes, pH 7.5, 5 mM MgSO<sub>A</sub>, 0.5% BSA), washed 4 times with ice-cold binding buffer without BSA, and incubated for 15 minutes with binding buffer without BSA containing 60ng/ml disuccinimidyl suberate at 4°C under constant rotation. 20 Crosslinking was terminated by addition of 7% sucrose in binding buffer. Cells were scraped, collected and pelleted by centrifugation, then resuspended in lysis buffer (10 mM Tris, pH 7.4, 1 mM EDTA, pH 8.0, 1% Triton-X 100, 10  $\mu$ g/ml of pepstatin, 10 $\mu$ g/ml leupeptin, 10  $\mu$ g/ml antipain, 100  $\mu$ g/m; benzamidine hydrochloride, 100  $\mu$ g/ml soybean trypsin inhibitor, 50  $\mu$ g/ml aprotonin, and 1 mM phenylmethylsulfonyl fluoride). Solubilized material was analyzed by 7% SDS-PAGE and subjected to

PCT/US92/09326 WO 93/09228

-27-

autoradiographic analysis by exposure to X-AR film (Kodak) at -70°C.

#### **Enzymatic Digestion**

Digestion of solubilized TGF-b receptors with chondroitinase and heparitinase was performed as described (Cheifetz, S. and J.L. Andres, J. Biol. Chem. 263:16984-16991 (1988); Segarini, P.R. and S.M. Seyedin, J. Biol. Chem., 263: 8366-8370 (1988).

#### Generation of Stable Cell Lines

L6 myoblasts were split 1:10 into 10 cm dishes and 10 . transfected the following day by the calcium phosphate method (Chen, C. and H. Okayama, Molec. Cell. Biol. 7:2745-2752 (1987)) with clones R3-OF or R3-OFF in the forward and reverse orientations in the vector pcDNA-neo 15 (InVitrogen). Cells were subjected to selection in the presence of G418 (Geneticin, GIBCO) for several weeks until individual colonies were visible by the naked eye. These clones were isolated and amplified.

#### RNA Blot Analyses

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Rat tissue polyadenylated mRNA was prepared by the lithium chloride/urea method (Auffrey, C. and F. Raugeon, Eur. J. Biochemistry 107:303-313 (1980), followed by oligo-dT cellulose chromatography (Aviv and Leder, 1972). Polyadenylated mRNA from cell lines was prepared by the 25 proteinase K/SDS method (Gonda, T.J. et al., Molec. Cell. Biol. 2:617-624 (1982)). Samples of mRNA were resolved by electrophoresis on 1% agarose-2.2M formaldehyde gels, blotted onto nylon membranes (Biotrns, ICN) and incubated

-28-

with the 2.9 kb insert of clone Re-OF labeled with 32P by random priming as probe (Sambrook, J. et al., Molecular Cloning: A Laboratory Manual, 2d Ed., Cold Spring Harbor, NY, Cold Spring Harbor Laboratory Press, (1989). Hybridizations were performed at 42°C in hybridization buffer containing 50% formamide overnight, and blots were washed at 55°C in 0.2X SSC, 0.1% SDS, before exposure to X-AR film at -70°C.

Example 1. Production of Anti-Type III Receptor Protein

Antibodies and Microsequencing and Microsequencing of Peptides Resulting from Partial

Proteolysis of Purified Type III Receptor

Initially cellular proteoglycans were purified from human placenta and then subjected to enzymatic deglycosy-15 lation with heparitinase and chondroitinase. Protein cores in the molecular weight range of 100-130 kilodaltons were further purified by preparative gel electrophoresis; these should include the type III receptor. This partially purified material was used as an immunogen in mice. After screening 850 hybridoma lines developed from immunized mice, three lines were found to produce antibodies that specifically recognized and immunoprecipitated a deglycosylated polypeptide species of 100-120 kD. This species could be radiolabelled by incubation of whole cells with  $^{125}I-TGF-\beta$  followed by covalent cross-linking. Its size is consistent with that of the protein core previously reported for the type III receptor. (Massague, J., Annu. Rev. Cell. Biol. 6:597-641 (1990))

Monoclonal antibody 94 was used to purify the type III receptor from rat liver by affinity-chromatography. The purified receptor was subjected to partial protectysis and the resulting peptides were resolved by high pressure liquid chromatography. Several peptides were subjected to microsequencing and yielded the following oligopeptide sequences:

Peptide I: ILLDPDHPPAL (SEQ ID NO. 5)

Peptide II: QAPFPINFMIA (SEQ ID NO. 6)

10 Peptide III: QPIVPSVQ (SEQ ID NO. 7)

Peptide IV: FYVEQGYGR (SEQ ID NO. 8)

These peptide sequences were used to construct degenerate oligonucleotides that served either as primers in a cloning strategy using the polymerase chain reaction (PCR) or as probes in screening cDNA libraries. While this strategy was not productive, the oligopeptide sequences proved useful in verifying the receptor clones isolated by the second, alternative strategy (see Example 2).

## 20 Example 2. Expression Cloning of the Type III Receptor CDNA

An expression cloning strategy in COS cells, a procedure which takes advantage of the considerable amplification of individual cDNAs in transfected COS cells was used as an alternative means to isolate TGF-β receptor clones. Such amplification is mediated by SV40 large T antigen expressed by the COS cells interacting

PCT/US92/09326 WO 93/09228

with a SV40 origin of replication in the cDNA vector. Gearing, D. et al., EMBO J. 8:3667-3676 (1989); Lin, . H.Y., et al., Proc. Natl. Acad. Sci. 88:3185-3189 (1991a); Lin, H. Y. et al., Science, in press (1991); Mathews, L. S. and Vale, W. W., Cell 65:973-982 (1991).

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The strategy involved the construction of a cDNA library from A-10 cells, a rat vascular smooth muscle cell line that expresses all three high-affinity TGF-etareceptors. The resulting cDNAs were inserted into the vector pcDNA-1, which carries the CMV transcriptional 10 promoter and the SV40 origin of replication. The resulting library was then divided into pools of 10,000 independent recombinants each and DNA from each pool was transfected into 1.5 x 10 COS-7 cells grown on glass flaskettes by means of DEAE-dextran transfection proce-15 dure. Aruffo, A. and Seed, B., Proc. Natl. Acad. Sci., U.S.A. 84:8573-8577 (1987); Gearing, D. et al., EMBO J. 8:3667-3676 (1989); Mathews, L. S. and Vale, W. W., Cell 65:973-982 (1991). The transfected cells were cultured for 48-60 hours and then exposed to radiolabelled TGF- $\beta$ 1 20 for four hours. Following this treatment, the glass slides carrying these cells were washed extensively and fixed. These slides were dipped in liquid photographic emulsion and examined by darkfield microscopy. While all of the receptor genes cloned to date by this procedure have undetectable or low constitutive levels of expression in COS cells, we were hindered by the fact that untransfected COS cells already express substantial amounts of type III TGF- $\beta$  receptor. Such expression, estimated to be approximately 2 x 105 receptor molecules per cell, might well have generated an unacceptably high level of background binding. However, since the detection procedure involves visualizing radiolabelled

ligand-binding on individual cells, it was hoped that identifying occasional cells expressing substantially higher levels of vector-encoded receptor would be possible. This hope was vindicated in the initial experiments.

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After screening nearly one million cDNA clones in this manner, a glass slide containing 20 positive transfectants was identified. The original pool of expression constructs from which one such transfectant was derived was split into 25 subpools of 1000 clones each and these 10 were subjected to a second round of screening. further rounds of sib-selection resulted in the isolation of a cDNA clone (R3-0F) with a 2.9 kb insert that induced high levels of  $TGF-\beta$ -binding proteins in approximately 10% of COS cells into which it was transfected.

The specificity of this binding was validated by showing that addition of a 200-fold excess of unlabeled TGF- $\beta$  competitor strongly reduced binding of  $^{12.5}$ I-TGF- $\beta$ to transfected cells. By taking into account a transfection efficiency of 10% and the high background of 20 endogenous receptor expression, we calculated that the level of total 125 I-TGF-8 binding to each glass slide of cells transfected with this cDNA clone (Figure 1C) was only 2-fold above the level seen with mock transfectants (data not shown). Nonetheless, this marginal increase in 25 ligand-binding was sufficient to identify rare transfectants amidst a large field of cells expressing this background level of receptor.

The R3-OF cDNA encoded an open reading frame of 836 amino acid residues of which the 3' most 18 were encoded 30 by vector sequence, clearly indicating that clone R3-OF

was an incomplete cDNA insert which ended prematurely at the codon specifying alanine 818 (Figure 4). R3-OF was used as a probe to isolate a full-length cDNA from a rat 208F lambda phage library. This clone, termed R3-OFF, was 6 kb in length and encoded a protein of 853 amino acids; its sequence was co-linear with that of clone R3-OF.

# Example 3. Characterization of the Product of the Full Length Clone R3-OFF

Characterization of the product of the full length clone R3-OFF was undertaken in order to determine which of the three TGF-β receptors it specified. To do so, COS transfectants were incubated with radioiodinated TGF-β, chemical crosslinker was added and the labelled receptors were resolved by polyacrylamide gel electrophoresis.

Labelling of cell surface TGF-β receptors in this way resulted in the detection of three distinct species on the surface of COS cells, as extensively by others (Massague, J. et al., Ann. NY Acad. Sci. 593:59-72

20 (1990). These included the two lower molecular weight type I and II receptors (65 and 85 kD) and the higher molecular weight type III proteoglycan, which migrated as a diffuse band of 280-330 kd. Enzymatic treatment of the proteoglycan with chondroitinase and heparitinase yielded a core protein of approximately 100 kd. Binding to all three receptor types was specific, in that it was completed by 200-fold excess of unlabeled TGF-β1.

Transfecting the R3-OFF cDNA caused a two-fold increase in expression of the type III receptor. When a cell lysate derived from COS cells transfected with clone

R3-OFF was treated with deglycosylating enzymes, the heterogenous 280-330 kd band was converted to a protein core which co-migrated with the type III protein core seen in untransfected A10 cells. Importantly, the recombinant protein core migrates differently from the endogenous COS cell type III protein core.

These observations were confirmed and extended in experiments using stably transfected cells expressing the R3-OFF cDNA. L6 rat skeleton muscle myoblasts normally do not express detectable type III mRNA or endogenous type III receptor (determined by radiolabelled ligand-binding assay). Such cells were transfected with the isolated cDNA in the vector pcDNA-neo. Cell clones stably expressing this clone in both the forward and reverse orientations with respect to the CMV promoter were isolated and analyzed by ligand-binding assay.

Introduction of either the full length clone R3-OFF or the partial clone R3-OF in the forward orientation led to the de novo expression of the type III receptor. L6 cells transfected with the cDNA in reversed orientation did not express this protein. The apparent size of the protein core of the type III receptor in cells transfected with the R3-OF clone is smaller than that expressed by R3-OFF transfected cells, consistent with the difference in the sizes of the protein cores predicted from the respective nucleic acid sequences (Figure 1).

Unexpectedly, the amount of radio-labelled ligand corss-linked to the type II receptor is increased by 2.5 fold in cells expressing the type III cDNA, while the amount cross-linked to the type I receptor remained

unchanged. This apparent specific up-regulation of ligand-binding to the type II receptor could be detected with all of the 15 stably transfected L6 cell lines analyzed so far. This effect seems to be mediated by the truncated clone R3-OF which lacks the cytoplasmic domain as well as by the full-length clone R3-OFF.

## Example 4. Expression of Type III Receptor

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Northern blot analysis demonstrated that the type III receptor mRNA is expressed as a single 6 kb message in several rat tissues. The level of mRNA expression in the liver was less than in other tissues, a result expected from earlier surveys of various tissues using radioiodinated TGF- $\beta$ 1. Based on this information, it appears that clone R3-OFF, with a ~6 kb cDNA insert, represents a full length rat type III cDNA clone.

Cells of mouse origin (MEL and YH16) appear to express a smaller (~5.5 kb) message for the type III mRNA than those of pig, rat and human origin. In all of these cells, expression or absence of the type III mRNA is consistent with the expression or absence of detectable 20 cell surface type III receptors with the notable exception of the retinoblastoma cell lines (Y79, Weri-1, Weri-24, and Weri-27). These cells have previously been shown to lack detectable surface expression of type III receptor, a result confirmed by our own unpublished work. It is striking that the type III receptor mRNA is expressed in these cells at a level comparable to that of other cells that do indeed express type III receptor proteins at readily detectable levels. At this moment, we can only conclude that TGF- $\beta$  receptor III expression, 30

which is substantial in normal retinoblasts (AD12), has been down-regulated in these retinoblastoma tumor cells, perhaps through post-transcriptional mechanisms.

# Example 5. Sequence Analysis of the Full-Length Type III cDNA

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The full-length cDNA clone (R3-OFF), described in Example 4, was subjected to sequence analysis. The full reading frame along with flanking sequences is presented in Figure 1. This reading frame encodes a protein of 853 amino acid residues, which is compatible with the 100 kD observed for the fully deglycosylated  $TGF-\beta$  type III receptor.

Two segments of derived protein sequence (underlined and italicized, residues 378-388 and 427-434) precisely

15 match those determined earlier from direct biochemical analysis of the purified receptor protein. This further secured the identity of this isolated cDNA clone as encoding the rat type III receptor.

This TGF-β binding protein has an unusual structure

for a cytokine receptor. Hydropathy analysis indicates a
N-terminal signal sequence, followed by a long,
hydrophilic N-terminal region (Kyte, J. and R. F.

Doolittle, J. Mol. Biol. 157:105-132 (1982)). A 27
residue region of strong hydrophobicity (underlined,
residues 786-812) toward the C-terminus represents the
single putative transmembrane domain. This suggests that
nearly all of the receptor is composed of an N-terminal
extracellular domain that is anchored to the plasma
membrane near its C-terminus. A relatively short

C-terminal tail of 41 residues represents the putative cytoplasmic domain.

The clone R3-OF was also analyzed and found to be a truncated version of R3-OFF, with an identical open reading frame but whose last encoded residue is alanine 818 (Figure 1).

In R3-OFF there are six consensus N-linked glycosylation sites and 15 cysteines (indicated in Figure 1). There is at least one consensus glycosaminoglycan addition site at serine 535 (Bernfield, M. and K. C. Hooper, Ann. N.Y. Acad. Sci. in press (1991), and numerous Ser-Gly residues that are potential sites for GAG conjugation. A consensus protein kinase C site is also present at residue 817.

Only one other gene described to date, a 15 glycoprotein expressed in high quantities by endothelial cells and termed endoglin (Gougos and Letarte, 1990), contains a related amino acid sequence. Overall, there is -30% identity with the type III receptor over the entire 645 amino acid residue length of endoglin. 20 most homologous regions between the sequences of the type III receptor and endoglin (74% identity) falls primarily in the putative transmembrane and cytoplasmic domains. Similar to the general structure of type III receptor, endoglin is a glycoprotein which contains a large 25 hydrophilic and presumably extracellular N-terminal domain followed by a putative transmembrane domain and a short cytoplasmic tail of 47 amino acid residues. The biological role of endoglin is unclear, though it has been suggested that it may involve cell-cell recognition 30 through interactions of an "RGD" sequence on its

ectodomain with other adhesion molecules. Unlike the  $TGF-\beta$  type III receptor, endoglin does not carry GAG groups.

#### Equivalents

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Those skilled in the art will recognize, or be able to ascertain using not more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

International Application No: PCT/

MICROOR	GANISMS
Optional Shoet in connection with the microorganism reterred to on	page 6 Inc 12 of the description 2
A. IDENTIFICATION OF DEPOSIT	
Further deposits are identified on an additional sheet 3	
Name of depositary institution 4	
American Type Culture Colle	ction
Address of depositary institution (including posts) code and country	)•
12301 Parklawn Drive Rockville, Maryland 20852	USA
Date of deposit *	Accession Number 6
21 October 1991	75127
B. ADDITIONAL INDICATIONS ! (leave blank if not applicable	n which a European Patent is sought,
the Applicant hereby informs the European Rule 28(4) that, until the grant of the European Patent or un Application has been refused or is withdrawn, the availability of the the American Type Culture Collectic shall be effected only by the issuby the requester in accordance with C. DESIGNATED STATES FOR WHICH INDICATIONS ARE Europe (EP) Australia Canada Japan	e publication of the mention of the til the date on which the European withdrawn or is deemed to be biological material deposited withou under Accession No. e of a sample to an expert nominated h European Rule 28(5).
D. SEPARATE FURNISHING OF INDICATIONS (leave blan	
The indications listed below will be authorized to the international "Accession Number of Deposit")	Bureau later * (Specify the general nature of the indications e.g.,
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E. This sheet was received with the international application wi	non filed (to be checked by the receiving Office)  LINIE L. BONNER  INTERNATIONAL DIVISION  (Authorized Officer)
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ues	(Authorized Officer)

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-39-

#### CLAIMS

- 1. Isolated DNA encoding TGF- $\beta$  receptor of vertebrate origin or DNA which hybridizes thereto and encodes TGF- $\beta$  receptor of vertebrate origin.
- 5 2. Isolated DNA of Claim 1 wherein the TGF- $\beta$  receptor is TGF- $\beta$  type III receptor or TGF- $\beta$  type II receptor.
  - 3. Isolated DNA of Claim 2 which is of mammalian origin.
- 10 4. Isolated DNA of murine or human origin encoding  $TGF-\beta$  type III receptor or DNA which hybridizes thereto.
- Isolated DNA of Claim 4 having the nucleotide sequence of Figure 1 or a portion thereof sufficient to encode TGF-β type III receptor.
- 6. Isolated DNA of murine or human origin encoding  $TGF-\beta$  type II receptor or DNA which hybridizes thereto.
- Isolated DNA of Claim 6 having the nucleotide
   sequence of Figure 2 or a portion thereof sufficient to encode TGF-β type II receptor.
  - 8. Isolated TGF- $\beta$  type III receptor of mammalian origin.

- 40 -

- 9. Isolated TGF-β type III receptor of Claim 8 having the amino acid sequence of Figure 1 or a substantially similar amino acid sequence.
- 10. Isolated TGF- $\beta$  type II receptor of mammalian origin.
- 5 11. Isolated TGF- $\beta$  type II receptor of Claim 10 having the amino acid sequence of Figure 3 or a substantially similar amino acid sequence.
  - 12. Recombinant TGF- $\beta$  type III receptor of mammalian origin.
- 10 13. Recombinant TGF-β type III receptor of Claim 8 having the amino acid sequence of Figure 1 or a substantially similar amino acid sequence.
  - 14. Recombinant TGF- $\beta$  type II receptor of mammalian origin.
- 15 15. Recombinant TGF-β type II receptor of Claim 10 having the amino acid sequence of Figure 4 or a substantially similar amino acid sequence.
  - 16. Soluble TGF- $\beta$  receptor.
- 17. Soluble TGF- $\beta$  receptor of Claim 16 which is soluble 20 TGF- $\beta$  type III receptor.
  - 18. Soluble TGF-β type III receptor of Claim 17 in which the amino acid sequence is amino acids 1 through

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785, inclusive, of Figure 1 or a substantially similar amino acid sequence.

- 19. Soluble TGF- $\beta$  receptor of Claim 16 which is soluble TGF- $\beta$  type II receptor.
- 5 20. Soluble TGF- $\beta$  receptor of Claim 19 in which the amino acid sequence is approximately amino acids 1 through 166, inclusive, of Figure 3, or a substantially similar amino acid sequence.
- 21. An antibody which specifically recognized TGF-β type 10 III receptor of mammalian origin.
- 22. An antibody of Claim 21 which is a monoclonal .....antibody.
  - 23. An antibody which specifically recognizes soluble TGF- $\beta$  type III receptor of mammalian origin.
    - 15 24. An antibody which specifically recognizes soluble TGF-\$\beta\$ type II receptor of mammalian origin.
- 25. A method of altering TGF- $\beta$  binding to TGF- $\beta$  type II or type III receptor on the surface of a cell, comprising combining soluble TGF-β type II or type III receptor with the cell, under conditions appropriate for binding of the soluble TGF- $\beta$ receptor and  $TGF-\beta$ .

- 26. The method of Claim 25 wherein TGF- $\beta$  binding is inhibited.
- 27. A method of altering TGF-β binding to TGF-β type III receptor on the surface of a cell comprising combining the cell with DNA encoding TGF-β type III receptor in an appropriate expression system which expresses TGF-β type III receptor, under conditions appropriate for expression of TGF-β type III receptor and binding of TGF-β with TGF-β type III receptor.
- 28. A method of regulating the effect of TGF-β in a mammal, comprising administering to the mammal a TGF-β receptor selected from the group consisting of: TGF-β type III receptor, TGF-β type II receptor, soluble TGF-β type III receptor, soluble TGF-β type III receptor, TGF-β bound to TGF-β type III receptor or a combination thereof, in sufficient quantity to alter binding of TGF-β to TGF-β type III receptor, binding of TGF-β type II receptor or both.

- 29. TGF- $\beta$  receptor according to any one of Claims 8 to 20, for use in therapy.
- 30. An antibody according to any one of Claims 21 to 24, for use in therapy.
- 31. Use of TGF- $\beta$  receptor according to any one of Claims 8 to 20, for the manufacture of a medicament for altering (e.g. inhibiting) TGF- $\beta$  binding to TGF- $\beta$  type II or type III receptor on the surface of a cell.
- 10 32. Use of a TGF-β receptor selected from the group consisting of: TGF-β type III receptor, TGF-β type III receptor, soluble TGF-β type III receptor, soluble TGF-β type II receptor, TGF-β bound to TGF-β type III receptor or a combination thereof, for the manufacturing of a medicament for use in regulating the affect of TGF-β in a mammal.
- 33. A method of assessing the ability of a compound to interfere with TGF- $\beta$  binding to the TGF- $\beta$  type III receptor, comprising the steps of:
  - 20 a) combining:
    - 1) mammalian cells which express the TGF- $\beta$  type III receptor;
    - labeled TGF-β; and
    - a compound to be assessed;

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- b) maintaining the product of (a) under conditions sufficient for TGF- $\beta$  to bind to the TGF- $\beta$  type III receptor;
- c) determining the extent of binding of TGF- $\beta$  to TGF- $\beta$  type III receptors in the presence of the compound to be assessed; and
- d) comparing the determination made in (c) with the extent to which binding of TGF- $\beta$  to the TGF- $\beta$  type III receptor occurs in the absence of the compound to be assessed,

wherein if  $TGF-\beta$  binding to the  $TGF-\beta$  type III receptor occurs to a lesser extent in the presence of the compound to be assessed than in the absence of the compound to be assessed, the compound to be assessed interferes with  $TGF-\beta$  binding to  $TGF-\beta$  type III receptors.

- 34. A method of Claim 33 wherein the cells which express the TGF- $\beta$  type III receptor are a cell line.
- 35. A method of Claim 34 wherein the cells which express the TGF- $\beta$  type III receptor are cells modified to express the TGF- $\beta$  type III receptor.
  - 36. A method of Claim 35 wherein the cells modified to express the TGF- $\beta$  type III receptor are cells which have incorporated into them TGF- $\beta$  receptor cDNA in an appropriate vector or microinjected TGF- $\beta$  receptor RNA.

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- 37. A method of assessing the ability of a compound to interfere with  $TGF-\beta$  binding to the  $TGF-\beta$  type II receptor comprising the steps of:
  - a) combining:
    - 1) mammalian cells which express the TGF- $\beta$  type II receptor;
    - 2) labeled TGF- $\beta$ ; and
    - 3) a compound to be assessed;
- b) maintaining the product of (a) under conditions sufficient for TGF- $\beta$  to bind to the TGF- $\beta$  type II receptor;
  - c) determining the extent of binding of TGF- $\beta$  to TGF- $\beta$  type II receptors in the presence of the compound to be assessed; and
  - d) comparing the determination made in (c) with the extent to which binding of TGF-β to the TGF-β type II receptor occurs in the absence of the compound to be assessed,
- wherein if TGF-β binding to the TGF-β type II
  receptor occurs to a lesser extent in the presence
  of the compound to be assessed than in the absence
  of the compound to be assessed, the compound to be
  assessed has interfered with TGF-β binding to TGF-β
  type II receptor.
  - 25 38. A method of Claim 37 wherein the cells which express the  $TGF-\beta$  type II receptor are a cell line.
    - 39. A method of Claim 38 wherein the cells which express the TGF- $\beta$  type II receptor are cells modified to express the TGF- $\beta$  type II receptor.

40. A method of Claim 39 wherein the cells modified to express the TGF- $\beta$  type II receptor are cells which have incorporated into them TGF- $\beta$  receptor cDNA in an appropriate vector or microinjected TGF- $\beta$  receptor RNA.

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- 41. A method of detecting abnormal binding of TGF- $\beta$ TGF- $\beta$  type III receptors of TGF- $\beta$  type II receptors
  at a cell surface, comprising:
  - a) determining the extent of binding of TGF- $\beta$  to TGF- $\beta$  type III receptors or TGF- $\beta$  type II receptors by cells in a sample obtained from an individual in whom binding is to be assessed thereby producing a test binding value; and
  - b) comparing the results of (a) with the extent to which binding occurs at the cell surface in control cells which are cells known to have abnormal binding of TGF-β to TGF-β type III receptors or TGF-β type II receptors resulting in a control binding value,
- wherein a test binding value similar to the control binding value is indicative of abnormal binding of  $TGF-\beta$  to  $TGF-\beta$  type III receptor or  $TGF-\beta$  type II receptor.

1/7

#### FIGURE 1A

CAGGAGGTGA AAGTCCCCGG CGGTCCCGAT GGCCCATTG CACTGCGCTG CTGAGCTCGC -180 GGCGCCTGC GCACACTGGG GGGACTCGCT TCGGCTAGTA ACTCCTCCAC CTCGCGCGGG -120 AAGCACCGGTC CTGGACACGC TGCCTCCGAG GCAAGTTGAA CAGTCCCAGA AAGGATCTTA - 60 AAGCTACACC CGACTGCCA CGATTGCCT CAATCTGAAG AACCAAAGGC TGTTGGAGAG - 1  ATG GCA GTG ACA TCC CAC CAC ATG ATC CGG GTG ATG GTT GTC CTG ATG Met Ala Val Thr Ser His His Met 11e Pro Val Met Val Val Leu Met	-240	n															
GGCCGCCTGC GCACACTGGG GGGACTCGCT TCGGCTAGTA ACTCCTCCAC CTCGCGCGG -120 ACGACCGGTC CTGGGACACGC TGCCTGCGAG GCAAGTTGAA CAGTGCAGAG AAGGATCTTA - 60 AAGCTACACC CGACTGCCA CGATTGCCTT CAATCTGAAG AACCAAAGGC TGTTGGAGAG - 1  ATG GCA GTG ACA TCC CAC CAC ATG ATC CCG GTG ATG GTT GTC CTG ATG Met Ala Val Thr Ser His His Met Ile Pro Val Met Val Val Leu Met 16  AGC GCC TGC CTG GCC ACC GCC GGT CCA GAG CCC AGC ACC CGG TGT GAA 96 Ser Ala Cys Leu Ala Thr Ala Gly Pro Glu Pro Ser Thr Arg Cys Glu 32  CTG TCA CCA ATC AAC GCC TCT CAC CCA GTC CAG GCC TTG ATG GAA ACC Leu Ser Pro Ile Ass Ala Ser His Pro Val Gln Ala Leu Met Glu Ser 48  TTC ACC GTT CTG TCT GGC TGT GCC AGC AGC AGC ACC GGG CTG CCA 192 Phe Thr Val Leu Ser Gly Cys Ala Ser Arg Gly Thr Thr Gly Leu Pro 64  AGG GAG GTC CAT GTC CTA AAC CTC CGA AGT ACA GAT CAG GGA CCA GGC 240 Arg Glu Val His Val Leu Ass Leu Arg Ser Thr Asp Gln Gly Pro Gly 80  CAG CGG CAG AGA GAG GTT ACC CTG CAC CTG AAC CCC ATT GCC TGG GTG CAC GIN Arg Gln Arg Glu Val Thr Leu His Leu Ass Pro Ile Ala Ser Val 96  CAC ACT CAC CAC AAA CCT ATC GTG TTC CTG CTC CAC CTG GTG CGC CAC GCC CAC CAC CAC CAC CAC AGA GAA CCT CAC CAC CAC CAC CAC CAC CAC CAC C			rga i	AAGT	ccc	G CC	GTC	CGGAT	r GG(	CGCAC	TTG	CACT	rgcgo	CTG	CTGA	CTCGC	-180
ARGCTACACC CGACTGCCA CGATTGCCT CAATCTGAAG AACCAAAGGC TGTTGGAGAG - 1  ATG GCA GTG ACA TCC CAC CAC ATG ATC CCG GTG ATG GTT GTC CTG ATG Met Ala Val Thr Ser His His Met 11e Pro Val Met Val Val Leu Met 16  AGC GCC TGC GCC ACC GCC GGT CCA GAG CCC AGC ACC CGG TGT GAA 96 Ser Ala Cys Leu Ala Thr Ala Gly Pro Glu Pro Ser Thr Arg Cys Glu 32  T  CTG TCA CCA ATC AAC GCC TCT CAC CCA GTC CAG GCC TTG ATG GAA AGC ACC CGG TGT GAA 32  TTC ACC GTT CTG TCT GGC TGT GCC AGC AGA GGC ACC AGC AGC AGC AGC AGC	GGC	CGCC:	rgc (	CAC	ACTG	G GC	GAC	rcgc1	r TCC	GCT	AGTA	ACTO	CTC	CAC	CTCG	CGGCGG	-120
ATG GCA GTG ACA TCC CAC CAC ATG ATC CCG GTG ATG GTT GTC CTG ATG  Met Ala Val Thr Ser His His Met Ile Pro Val Met Val Val Leu Met  AGC GCC TGC CTG GCC ACC GCC GGT CCA GAG CCC AGC ACC CGG TGT GAA  Ser Ala Cys Leu Ala Thr Ala Gly Pro Glu Pro Ser Thr Arg Cys Glu  2  CTG TCA CCA ATC AAC GCC TCT CAC CCA GTC CAG GCC TTG ATG GAA  Ser Pro Ile Asn Ala Ser His Pro Val Gln Ala Leu Met Glu Ser  TTC ACC GTT CTG TCT GGC TGT GCC AGC AGC ACC ACC GGG CTG CCA  Phe Thr Val Leu Ser Gly Cys Ala Ser Arg Gly Thr Thr Gly Leu Pro  AGG GAG GTC CAT GTC CTA AAC CTC CGA AGT ACA GAT CAG GGA CCA GGC  Arg Glu Val His Val Leu Asn Leu Arg Ser Thr Asp Gln Gly Pro Gly  80  CAG CGG CAG AGA GAG GTT ACC CTG CAC CTG AAC CCC ATT GCC TCG GTG  CAC ACT CAC CAC AAA CCT ATC GTG TTC CTG CTC AAC CCC ATT GCC TCG GTG  CAC ACT CAC CAC AAA CCT ATC GTG TTC CTG CTC AAC TCC CCC CAG CCC  His Thr His His Lys Pro Ile Val Phe Leu Leu Asn Ser Pro Gln Pro  112  CTC GTG TGG CAT CTG AAG ACG GAG AGA CTG CCC GCT GTT CCC CAG ACC  CTC CTC CTG GTT TCG GAG GGT TCT GTG GTC CAG TTT CCA TCA GAA AAC  Leu Val Trp His Leu Lys Thr Glu Arg Leu Ala Ala Gly Val Pro Arg  128  CTC TTC CTG GTT TCG GAG GGT TCT GTG GTC CAG TTT CCA TCA GGA AAC  Leu Val Trp His Leu Lys Thr Glu Arg Leu Ala Ala Gly Val Pro Arg  128  CTC TTC CTG GTT TCG GAG GGT TCT GTG GTC CAG TTT CCA TCA GGA AAC  Leu Phe Leu Val Ser Glu Gly Ser Val Val Gln Phe Pro Ser Gly Asn  148  TTC TCC TTG ACA CCA GAA ACA GAG GAA AGG GAA AGG GAA TTT CCA TCA GGA AAC  CAAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  TTC GAT GAA CTC AAG ATA GCA AAG AAC ATC TAT ATT AAA GTG GAA AAT  TTC ACT GAA CTC AAG ATA GCA AAC AGA AAC ATC TAT ATT AAA GTG GAA  TTC ACT GAA CTC AAG ATA GCA AAC AGA AAC ATC TAT ATT ATT ATT ATT TATA ATT T	ACG	ACCG	GTC (	CTGG	ACAC	C TO	CCT	CGAC	GCI	\AGT	MAD	CAG	rgcac	GAG :	<b>AAGG</b>	atctta	- 60
Met Ala Val Thr Ser His His Met Ile Pro Val Met Val Val Leu Met  AGC GCC TGC CTG GCC ACC GCC GGT CCA GAG CCC AGC ACC CGG TGT GAA  Ser Ala Cys Leu Ala Thr Ala Gly Pro Glu Pro Ser Thr Arg Cys Glu  32  CTG TCA CCA ATC AAC GCC TCT CAC CCA GTC CAG GCC TTG ATG GAG AGC  Leu Ser Pro Ile Asn Ala Ser His Pro Val Gln Ala Leu Met Glu Ser  AGC GTT CTG TCT GGC TGT GCC AGC AGA GGC ACC ACC ACC GGG CTG CCA  Phe Thr Val Leu Ser Gly Cys Ala Ser Arg Gly Thr Thr Gly Leu Pro  AGG GAG GTC CAT GTC CTA AAC CTC CGA AGT ACA GAT CAG GGA CCA GGC  Arg Glu Val His Val Leu Asn Leu Arg Ser Thr Asp Gln Gly Pro Gly  CAG CGG CAG AGA GAG GTT ACC CTG CAC CTG AAC CCC ATT GCC TGG GTG  CAC ACT CAC CAC AAA CCT ATC CTG TTC CTG CTC AAC TCC CCC CAG  CACT CAC CAC AAA CCT ATC GTG TTC CTG CTC AAC TCC CCC CAG  CACT CAC CAC AAA CCT ATC GTG TTC CTG CTC AAC TCC CCC CAG  CAC ACT CAC CAC AAA CCT ATC GTG TTC CTG CTC CAC GTC CCC CAG  CAC TCG CAC CAC AAA CCT ATC GTG TTC CTG CTC CAC TCC CCC CAG  CAC TCG CAC CAC AAA CCT ATC GTG TTC CTG CTC CAC TCC CCC CAG  CCG GTG TGG CAT CTG AAG ACC GAG AGA CTG CCC GTG TC CCC CAG  CCT CTC TCT GTG TCC GAG GGT TCT GTG GTC CCC GTT GTC CCC AGA  Leu Val Trp His Leu Lys Thr Glu Arg Leu Ala Ala Gly Val Pro Arg  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAC  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAT  A80  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  TTC GAT GAA CTC AAG ATA GCA AGA AAC ATC TAT ATT AAA GTG GGA GAA  576	AAG	CTAC	ACC (	CGAC:	rtgc	CA CO	TTA	CCT	CA)	TCT	BAAG	AAC	CAAAC	GC '	TGTT	GGAGAG	- 1
Met Ala Val Thr Ser His His Met Ile Pro Val Met Val Val Leu Met  AGC GCC TGC CTG GCC ACC GCC GGT CCA GAG CCC AGC ACC CGG TGT GAA  Ser Ala Cys Leu Ala Thr Ala Gly Pro Glu Pro Ser Thr Arg Cys Glu  32  CTG TCA CCA ATC AAC GCC TCT CAC CCA GTC CAG GCC TTG ATG GAG AGC  Leu Ser Pro Ile Asn Ala Ser His Pro Val Gln Ala Leu Met Glu Ser  AGC GTT CTG TCT GGC TGT GCC AGC AGA GGC ACC ACC ACC GGG CTG CCA  Phe Thr Val Leu Ser Gly Cys Ala Ser Arg Gly Thr Thr Gly Leu Pro  AGG GAG GTC CAT GTC CTA AAC CTC CGA AGT ACA GAT CAG GGA CCA GGC  Arg Glu Val His Val Leu Asn Leu Arg Ser Thr Asp Gln Gly Pro Gly  CAG CGG CAG AGA GAG GTT ACC CTG CAC CTG AAC CCC ATT GCC TGG GTG  CAC ACT CAC CAC AAA CCT ATC CTG TTC CTG CTC AAC TCC CCC CAG  CACT CAC CAC AAA CCT ATC GTG TTC CTG CTC AAC TCC CCC CAG  CACT CAC CAC AAA CCT ATC GTG TTC CTG CTC AAC TCC CCC CAG  CAC ACT CAC CAC AAA CCT ATC GTG TTC CTG CTC CAC GTC CCC CAG  CAC TCG CAC CAC AAA CCT ATC GTG TTC CTG CTC CAC TCC CCC CAG  CAC TCG CAC CAC AAA CCT ATC GTG TTC CTG CTC CAC TCC CCC CAG  CCG GTG TGG CAT CTG AAG ACC GAG AGA CTG CCC GTG TC CCC CAG  CCT CTC TCT GTG TCC GAG GGT TCT GTG GTC CCC GTT GTC CCC AGA  Leu Val Trp His Leu Lys Thr Glu Arg Leu Ala Ala Gly Val Pro Arg  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAC  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAT  A80  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  TTC GAT GAA CTC AAG ATA GCA AGA AAC ATC TAT ATT AAA GTG GGA GAA  576																	
Met Ala Val Thr Ser His His Met Ile Pro Val Met Val Val Leu Met  AGC GCC TGC CTG GCC ACC GCC GGT CCA GAG CCC AGC ACC CGG TGT GAA  Ser Ala Cys Leu Ala Thr Ala Gly Pro Glu Pro Ser Thr Arg Cys Glu  32  CTG TCA CCA ATC AAC GCC TCT CAC CCA GTC CAG GCC TTG ATG GAG AGC  Leu Ser Pro Ile Asn Ala Ser His Pro Val Gln Ala Leu Met Glu Ser  AGC GTT CTG TCT GGC TGT GCC AGC AGA GGC ACC ACC ACC GGG CTG CCA  Phe Thr Val Leu Ser Gly Cys Ala Ser Arg Gly Thr Thr Gly Leu Pro  AGG GAG GTC CAT GTC CTA AAC CTC CGA AGT ACA GAT CAG GGA CCA GGC  Arg Glu Val His Val Leu Asn Leu Arg Ser Thr Asp Gln Gly Pro Gly  CAG CGG CAG AGA GAG GTT ACC CTG CAC CTG AAC CCC ATT GCC TGG GTG  CAC ACT CAC CAC AAA CCT ATC CTG TTC CTG CTC AAC TCC CCC CAG  CACT CAC CAC AAA CCT ATC GTG TTC CTG CTC AAC TCC CCC CAG  CACT CAC CAC AAA CCT ATC GTG TTC CTG CTC AAC TCC CCC CAG  CAC ACT CAC CAC AAA CCT ATC GTG TTC CTG CTC CAC GTC CCC CAG  CAC TCG CAC CAC AAA CCT ATC GTG TTC CTG CTC CAC TCC CCC CAG  CAC TCG CAC CAC AAA CCT ATC GTG TTC CTG CTC CAC TCC CCC CAG  CCG GTG TGG CAT CTG AAG ACC GAG AGA CTG CCC GTG TC CCC CAG  CCT CTC TCT GTG TCC GAG GGT TCT GTG GTC CCC GTT GTC CCC AGA  Leu Val Trp His Leu Lys Thr Glu Arg Leu Ala Ala Gly Val Pro Arg  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAC  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAT  A80  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  TTC GAT GAA CTC AAG ATA GCA AGA AAC ATC TAT ATT AAA GTG GGA GAA  576												3 mc		C.P.C	~~~	N TOC	AΩ
AGC GCC TGC CTC GCC ACC GCC GGT CCA GAG CCC AGC ACC CGG TGT GAA Ser Ala Cys Leu Ala Thr Ala Gly Pro Glu Pro Ser Thr Arg Cys Glu  CTG TCA CCA ATC AAC GCC TCT CAC CCA GTC CAG GCC TTG ATG GAA ACC Leu Ser Pro Ile Asn Ala Ser His Pro Val Gln Ala Leu Met Glu Ser  TTC ACC GTT CTG TCT GGC TGT GCC AGC AGC AGA GGC ACC ACC GGG CTG CCA Phe Thr Val Leu Ser Gly Cys Ala Ser Arg Gly Thr Thr Gly Leu Pro  AGG GAG GTC CAT GTC CTA AAC CTC CGA AGT ACA GAT CAG GGA CCA GGC Arg Glu Val His Val Leu Asn Leu Arg Ser Thr Asp Gln Gly Pro Gly  CAG CGG CAG AGA GAG GTT ACC CTG CAC CTG AAC CCC ATT GCC TCG GTG CAC ACT CAC CAC AAA CCT ATC GTG TTC CTG CTC AAC CCC ATT GCC TCG GTG CAC ACT CAC CAC AAA CCT ATC GTG TTC CTG CTC AAC TCC CCC CAG CCC ACT CAC CAC CAC AAA CCT ATC GTG TTC CTG CTC CCC CAG CCC ACT CGC CAT CTC AAG ACC GAG AGA CTG GCC GCT GGT GTC CCC AGA Leu Val Trp His Leu Lys Thr Glu Arg Leu Ala Ala Gly Val Pro Arg  CTC TTC CTG GTT TCC GAG GGT TCT GTG GTC CAG TTT CCA TCA CGA AAC  TTC CTC TTG ACA GCA GAA ACA GAG GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAT  TTC TCC TTG ACA GCA GAA ACA GAG GAA ACA GAG GAA TAT GGA GCA GTG ACT TCG GTG TGG CGC TGG GCC CAA AAC GAG GAA ACC AAC GAC GCA GCA	ATG	GCA	GTG	ACA	TCC	CAC	CAC	ATG	ATC	Des	U1G	Mot	Uni	Ual	Tou	Mot	
SET Ala Cys Leu Ala Thr Ala Gly Pro Glu Pro Ser Thr Arg Cys Glu  TO TCA CCA ATC AAC GCC TCT CAC CCA GTC CAG GCC TTG ATG GAG AGC Leu Ser Pro Ile Asn Ala Ser His Pro Val Gln Ala Leu Met Glu Ser  TTC ACC GTT CTG TCT GGC TGT GCC AGC AGC AGA GGC ACC ACC GGG CTG CCA  AGG GAG GTC CAT GTC CTA AAC CTC CGA AGT ACA GAT CAG GGA CCA GGC  AGG GAG GTC CAT GTC CTA AAC CTC CGA AGT ACA GAT CAG GGA CCA GGC  ARG GAG GTC CAT GTC CTA AAC CTC CGA AGT ACA GAT CAG GGA CCA GGC  ARG GAG GTC CAT GTC CTA AAC CTC CGA AGT ACA GAT CAG GGA CCA GGC  ARG GGG CAG AGA GAG GTT ACC CTG CAC CTG AAC CCC ATT GCC TCG GTG  CAG CGG CAG AGA GAG GTT ACC CTG CAC CTG AAC CCC ATT GCC TCG GTG  CAC ACT CAC CAC AAA CCT ATC GTG TTC CTG CTC AAC TCC CCC CAG CCC  AGT ATC GAC CAC AAA CCT ATC GTG TTC CTG CTC AAC TCC CCC CAG CCC  AGA CTC CAC CAC AAA CCT ATC GTG TTC CTG CTC AAC TCC CCC CAG CCC  AGA CTC CAC CAC AAA CCT ATC GTG TCC CTG CCC GGT GTC CCC AGA  Leu Val Trp His Leu Lys Thr Glu Arg Leu Ala Ala Gly Val Pro Arg  CTC TTC CTG GTT TCC GAG GGT TCT GTG GTC CAG TTT CCA TCA GGA AAC  Leu Val Trp His Leu Lys Thr Glu Arg Leu Ala Ala Gly Val Pro Arg  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAT  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAT  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAT  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA AAC ATC TAT ATT AAA GTG GGA GAA  TTC ACT GAA CTC AAG ATA GCA AGA AAC ATC TAT ATT AAA GTG GGA GAA  TTC ACT GAA CTC AAG ATA GCA AGA AAC ATC TAT TAT AAA GTG GGA GAA	Met	Ala	Val	Thr	Ser	HIB	HIB	Met	116	Pro	vai	net	ANT	Val	Leu	nec	10
SET Ala Cys Leu Ala Thr Ala Gly Pro Glu Pro Ser Thr Arg Cys Glu  TO TCA CCA ATC AAC GCC TCT CAC CCA GTC CAG GCC TTG ATG GAG AGC Leu Ser Pro Ile Asn Ala Ser His Pro Val Gln Ala Leu Met Glu Ser  TTC ACC GTT CTG TCT GGC TGT GCC AGC AGC AGA GGC ACC ACC GGG CTG CCA  AGG GAG GTC CAT GTC CTA AAC CTC CGA AGT ACA GAT CAG GGA CCA GGC  AGG GAG GTC CAT GTC CTA AAC CTC CGA AGT ACA GAT CAG GGA CCA GGC  ARG GAG GTC CAT GTC CTA AAC CTC CGA AGT ACA GAT CAG GGA CCA GGC  ARG GAG GTC CAT GTC CTA AAC CTC CGA AGT ACA GAT CAG GGA CCA GGC  ARG GGG CAG AGA GAG GTT ACC CTG CAC CTG AAC CCC ATT GCC TCG GTG  CAG CGG CAG AGA GAG GTT ACC CTG CAC CTG AAC CCC ATT GCC TCG GTG  CAC ACT CAC CAC AAA CCT ATC GTG TTC CTG CTC AAC TCC CCC CAG CCC  AGT ATC GAC CAC AAA CCT ATC GTG TTC CTG CTC AAC TCC CCC CAG CCC  AGA CTC CAC CAC AAA CCT ATC GTG TTC CTG CTC AAC TCC CCC CAG CCC  AGA CTC CAC CAC AAA CCT ATC GTG TCC CTG CCC GGT GTC CCC AGA  Leu Val Trp His Leu Lys Thr Glu Arg Leu Ala Ala Gly Val Pro Arg  CTC TTC CTG GTT TCC GAG GGT TCT GTG GTC CAG TTT CCA TCA GGA AAC  Leu Val Trp His Leu Lys Thr Glu Arg Leu Ala Ala Gly Val Pro Arg  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAT  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAT  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAT  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA AAC ATC TAT ATT AAA GTG GGA GAA  TTC ACT GAA CTC AAG ATA GCA AGA AAC ATC TAT ATT AAA GTG GGA GAA  TTC ACT GAA CTC AAG ATA GCA AGA AAC ATC TAT TAT AAA GTG GGA GAA	AGC	GCC	TGC	CTG	GCC	ACC	GCC	GGT	CCA	GAG	ccc	AGC	ACC	CGG	TGT	GAA	96
CTG TCA CCA ATC AAC GCC TCT CAC CCA GTC CAG GCC TTG ATG GAG AGC 144 Leu Ser Pro 11e Abn Ala Ser His Pro Val Gln Ala Leu Met Glu Ser 48  TTC ACC GTT CTG TCT GGC TGT GCC AGC AGC AGA GGC ACC GGG CTG CCA 192 Phe Thr Val Leu Ser Gly Cys Ala Ser Arg Gly Thr Thr Gly Leu Pro 64  AGG GAG GTC CAT GTC CTA AAC CTC CGA AGT ACA GAT CAG GGA CCA GGC 240 Arg Glu Val His Val Leu Abn Leu Arg Ser Thr Abp Gln Gly Pro Gly 80  CAG CGG CAG AGA GAG GTT ACC CTG CAC CTG AAC CCC ATT GCC TGG GTG 288 Gln Arg Gln Arg Glu Val Thr Leu His Leu Abn Pro 11e Ala Ser Val 96  CAC ACT CAC CAC AAA CCT ATC GTG TTC CTG CTC AAC TCC CCC CAG CCC 336 His Thr His His Lys Pro 11e Val Phe Leu Leu Abn Ser Pro Gln Pro 112  CTG GTG TGG CAT CTG AAG ACG GAG AGA CTG GCC GCT GGT GTC CCC AGA 384 Leu Val Trp His Leu Lys Thr Glu Arg Leu Ala Ala Gly Val Pro Arg 128  CTC TTC CTG GTT TCG GAG GGT TCT GTG GTC CAG TTT CCA TCA GGA AAC 432 Leu Phe Leu Val Ser Glu Gly Ser Val Val Gln Phe Pro Ser Gly Abn 144  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAT 480 Phe Ser Leu Thr Ala Glu Thr Glu Glu Arg Abn Phe Pro Gln Glu Abn 160  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA AAC ATC TAT ATT GGA GCA GTA CTT TCC TCC TCC AAC TCC GCC GCT GCT ACT TCC GCC GCT GCT ACT TCC TCC TCC ACC ACC ACC GCC GCT GCT GCT ACC TCC GCT ACC TCC CAC ACC ACC ACC ACC ACC ACC A	Ser	Ala	Cvs	Leu	Ala	Thr	Ala	Gly	Pro	Glu	Pro	Ser	Thr	Arg	Сув	Glu	32
Leu Ser Pro Ile Asn Ala Ser His Pro Val Gln Ala Leu Met Glu Ser  A68  TTC ACC GTT CTG TCT GGC TGT GCC AGC AGA AGA GGC ACC ACC GGG CTG CCA  Phe Thr Val Leu Ser Gly Cys Ala Ser Arg Gly Thr Thr Gly Leu Pro  A64  A66  A66  A67  A68  A68  A68  A68  A68							4	r _						_			
Leu Ser Pro Ile Asn Ala Ser His Pro Val Gln Ala Leu Met Glu Ser  A68  TTC ACC GTT CTG TCT GGC TGT GCC AGC AGA AGA GGC ACC ACC GGG CTG CCA  Phe Thr Val Leu Ser Gly Cys Ala Ser Arg Gly Thr Thr Gly Leu Pro  A64  A66  A66  A67  A68  A68  A68  A68  A68			•														
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TTC ACC GTT CTG TCT GGC TGT GCC AGC AGA GGC ACC ACC GGG CTG CCA  192 Phe Thr Val Leu Ser Gly Cys Ala Ser Arg Gly Thr Thr Gly Leu Pro  64  AGG GAG GTC CAT GTC CTA AAC CTC CGA AGT ACA GAT CAG GGA CCA GGC  Arg Glu Val His Val Leu Asn Leu Arg Ser Thr Asp Gln Gly Pro Gly  80  CAG CGG CAG AGA GAG GTT ACC CTG CAC CTG AAC CCC ATT GCC TGG GTG  CAC CAC CAC AAA CCT ATC GTG TTC CTC CTC AAC TCC CCC CAG CCC  His Thr His His Lys Pro Ile Val Phe Leu Leu Asn Ser Pro Gln Pro  112  CTG GTG TGG CAT CTG AAG ACG GAG AGA CTG GCC GCT GGT GTC CCC AGA  Leu Val Trp His Leu Lys Thr Glu Arg Leu Ala Ala Gly Val Pro Arg  128  CTC TTC CTG GTT TCG GAG GGT TCT GTG GTC CAG TTT CCA TCA GGA AAC  Leu Phe Leu Val Ser Glu Gly Ser Val Val Gln Phe Pro Ser Gly Asn  144  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAT  480 Phe Ser Leu Thr Ala Glu Thr Glu Glu Arg Asn Phe Pro Gln Glu Asn  160  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA AAC ATC TAT ATT AAA GTG GGA GAA  576	Leu	Ser	Pro	Ile	Asn	Ala	Ser	His	Pro	Val	Gln	Ala	Leu	Met	Glu	Ser	48
Phe Thr Val Leu Ser Gly Cys Ala Ser Arg Gly Thr Thr Gly Leu Pro  AGG GAG GTC CAT GTC CTA AAC CTC CGA AGT ACA GAT CAG GGA CCA GGC  Arg Glu Val His Val Leu Asn Leu Arg Ser Thr Asp Gln Gly Pro Gly  CAG CGG CAG AGA GAG GTT ACC CTG CAC CTG AAC CCC ATT GCC TCG GTG  Gln Arg Gln Arg Glu Val Thr Leu His Leu Asn Pro Ile Ala Ser Val  96  CAC ACT CAC CAC AAA CCT ATC GTG TTC CTG CTC AAC TCC CCC CAG CCC  His Thr His His Lys Pro Ile Val Phe Leu Leu Asn Ser Pro Gln Pro  112  CTG GTG TGG CAT CTG AAG ACG GAG AGA CTG GCC GCT GGT GTC CCC AGA  Leu Val Trp His Leu Lys Thr Glu Arg Leu Ala Ala Gly Val Pro Arg  128  CTC TTC CTG GTT TCG GAG GGT TCT GTG GTC CAG TTT CCA TCA GGA AAC  Leu Phe Leu Val Ser Glu Gly Ser Val Val Gln Phe Pro Ser Gly Asn  144  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAT  480  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  TTC ACT GAA CTC AAG ATA GCA AGA AAC ATC TAT ATT AAA GTG GGA GAA  576			•		#												
Phe Thr Val Leu Ser Gly Cys Ala Ser Arg Gly Thr Thr Gly Leu Pro  AGG GAG GTC CAT GTC CTA AAC CTC CGA AGT ACA GAT CAG GGA CCA GGC  Arg Glu Val His Val Leu Asn Leu Arg Ser Thr Asp Gln Gly Pro Gly  CAG CGG CAG AGA GAG GTT ACC CTG CAC CTG AAC CCC ATT GCC TCG GTG  Gln Arg Gln Arg Glu Val Thr Leu His Leu Asn Pro Ile Ala Ser Val  96  CAC ACT CAC CAC AAA CCT ATC GTG TTC CTG CTC AAC TCC CCC CAG CCC  His Thr His His Lys Pro Ile Val Phe Leu Leu Asn Ser Pro Gln Pro  112  CTG GTG TGG CAT CTG AAG ACG GAG AGA CTG GCC GCT GGT GTC CCC AGA  Leu Val Trp His Leu Lys Thr Glu Arg Leu Ala Ala Gly Val Pro Arg  128  CTC TTC CTG GTT TCG GAG GGT TCT GTG GTC CAG TTT CCA TCA GGA AAC  Leu Phe Leu Val Ser Glu Gly Ser Val Val Gln Phe Pro Ser Gly Asn  144  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAT  480  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  TTC ACT GAA CTC AAG ATA GCA AGA AAC ATC TAT ATT AAA GTG GGA GAA  576				-			mcm		200	ACA	ccc	200	»cc	ccc	CTG	CCA	192
AGG GAG GTC CAT GTC CTA AAC CTC CGA AGT ACA GAT CAG GGA CCA GGC 240 Arg Glu Val His Val Leu Asn Leu Arg Ser Thr Asp Gln Gly Pro Gly 80 CAG CGG CAG AGA GAG GGT ACC CTG CAC CTG AAC CCC ATT GCC TCG GTG 288 Gln Arg Gln Arg Glu Val Thr Leu Bis Leu Asn Pro Ile Ala Ser Val 96 CAC ACT CAC CAC AAA CCT ATC GTG TTC CTG CTC AAC TCC CCC CAG CCC 336 His Thr His His Lys Pro Ile Val Phe Leu Leu Asn Ser Pro Gln Pro 112 CTG GTG TGG CAT CTG AAC ACG GAG AGA CTG GCC GCT GGT GTC CCC AGA 384 Leu Val Trp His Leu Lys Thr Glu Arg Leu Ala Ala Gly Val Pro Arg 128 CTC TTC CTG GTT TCG GAG GGT TCT GTG GTC CAG TTT CCA TCA GGA AAC 432 Leu Phe Leu Val Ser Glu Gly Ser Val Val Gln Phe Pro Ser Gly Asn 144 ff  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAT 480 GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG 528 Glu His Leu Val Arg Trp Ala Gln Lys Glu Tyr Gly Ala Val Thr Ser 176 TTC ACT GAA CTC AAG ATA GCA AGA AAC ATC TAT AAA GTG GGA GAA 576	TTC	ACC	GIT	CIG	TCT	Clu	Cve	Ala	Sor	Ara	Glv	Thr	Thr	Glv	Leu	Pro	
AGG GAG GTC CAT GTC CTA AAC CTC CGA AGT ACA GAT CAG GGA CCA GGC 240 Arg Glu Val His Val Leu Asn Leu Arg Ser Thr Asp Gln Gly Pro Gly 80 CAG CGG CAG AGA GAG GTT ACC CTG CAC CTG AAC CCC ATT GCC TCG GTG 288 Gln Arg Gln Arg Glu Val Thr Leu Bis Leu Asn Pro IIe Ala Ser Val 96 CAC ACT CAC CAC AAA CCT ATC GTG TTC CTG CTC AAC TCC CCC CAG CCC 336 His Thr His His Lys Pro IIe Val Phe Leu Leu Asn Ser Pro Gln Pro 112 CTG GTG TGG CAT CTG AAG ACG GAG AGA CTG GCC GCT GGT GTC CCC AGA 384 Leu Val Trp His Leu Lys Thr Glu Arg Leu Ala Ala Gly Val Pro Arg 128 CTC TTC CTG GTT TCG GAG GGT TCT GTG GTC CAG TTT CCA TCA GGA AAC Leu Phe Leu Val Ser Glu Gly Ser Val Val Gln Phe Pro Ser Gly Asn 144 # #	Pne	THE	ANT	Ten	er +	GIY		AIG	<b>-</b>	9	<b>-</b> 23			,			
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CAG CGG CAG AGA GAG GTT ACC CTG CAC CTG AAC CCC ATT GCC TCG GTG 288 Gln Arg Gln Arg Glu Val Thr Leu His Leu Asn Pro Ile Ala Ser Val 96  CAC ACT CAC CAC AAA CCT ATC GTG TTC CTG CTC AAC TCC CCC CAG CCC 336 His Thr His His Lys Pro Ile Val Phe Leu Leu Asn Ser Pro Gln Pro 112  CTG GTG TGG CAT CTG AAG ACG GAG AGA CTG GCC GCT GGT GTC CCC AGA 284 Leu Val Trp His Leu Lys Thr Glu Arg Leu Ala Ala Gly Val Pro Arg 128  CTC TTC CTG GTT TCG GAG GGT TCT GTG GTC CAG TTT CCA TCA GGA AAC 432 Leu Phe Leu Val Ser Glu Gly Ser Val Val Gln Phe Pro Ser Gly Asn 144  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAT 480 Phe Ser Leu Thr Ala Glu Thr Glu Glu Arg Asn Phe Pro Gln Glu Asn 160  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG 528 Glu His Leu Val Arg Trp Ala Gln Lys Glu Tyr Gly Ala Val Thr Ser 176	AGG	GAG	GTC	CAT	GTC	CTA	AAC	CTC	CGA	AGT	ACA	GAT	CAG	GGA	CCA	GGC	240
Gln Arg Gln Arg Glu Val Thr Leu His Leu Asn Pro Ile Ala Ser Val  CAC ACT CAC CAC AAA CCT ATC GTG TTC CTG CTC AAC TCC CCC CAG CCC  His Thr His His Lys Pro Ile Val Phe Leu Leu Asn Ser Pro Gln Pro  CTG GTG TGG CAT CTG AAG ACG GAG AGA CTG GCC GCT GGT GTC CCC AGA  Leu Val Trp His Leu Lys Thr Glu Arg Leu Ala Ala Gly Val Pro Arg  CTC TTC CTG GTT TCG GAG GGT TCT GTG GTC CAG TTT CCA TCA GGA AAC  Leu Phe Leu Val Ser Glu Gly Ser Val Val Gln Phe Pro Ser Gly Asn  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAT  Phe Ser Leu Thr Ala Glu Thr Glu Glu Arg Asn Phe Pro Gln Glu Asn  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  TTC ACT GAA CTC AAG ATA GCA AGA AAC ATC TAT ATT AAA GTG GGA GAA  576	Arg	Glu	Val	His	Val	Leu	Asn	Leu	Arg	Ser	Thr	Asp	Gln	Gly	Pro	Gly	80
Gln Arg Gln Arg Glu Val Thr Leu His Leu Asn Pro Ile Ala Ser Val  CAC ACT CAC CAC AAA CCT ATC GTG TTC CTG CTC AAC TCC CCC CAG CCC  His Thr His His Lys Pro Ile Val Phe Leu Leu Asn Ser Pro Gln Pro  CTG GTG TGG CAT CTG AAG ACG GAG AGA CTG GCC GCT GGT GTC CCC AGA  Leu Val Trp His Leu Lys Thr Glu Arg Leu Ala Ala Gly Val Pro Arg  CTC TTC CTG GTT TCG GAG GGT TCT GTG GTC CAG TTT CCA TCA GGA AAC  Leu Phe Leu Val Ser Glu Gly Ser Val Val Gln Phe Pro Ser Gly Asn  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAT  Phe Ser Leu Thr Ala Glu Thr Glu Glu Arg Asn Phe Pro Gln Glu Asn  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  TTC ACT GAA CTC AAG ATA GCA AGA AAC ATC TAT ATT AAA GTG GGA GAA  576					•												
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His Thr His His Lys Pro Ile Val Phe Leu Leu Asn Ser Pro Gln Pro 112  CTG GTG TGG CAT CTG AAG ACG GAG AGA CTG GCC GCT GGT GTC CCC AGA 384  Leu Val Trp His Leu Lys Thr Glu Arg Leu Ala Ala Gly Val Pro Arg 128  CTC TTC CTG GTT TCG GAG GGT TCT GTG GTC CAG TTT CCA TCA GGA AAC 432  Leu Phe Leu Val Ser Glu Gly Ser Val Val Gln Phe Pro Ser Gly Asn 144  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAT 480  Phe Ser Leu Thr Ala Glu Thr Glu Glu Arg Asn Phe Pro Gln Glu Asn 160  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG 528  Glu His Leu Val Arg Trp Ala Gln Lys Glu Tyr Gly Ala Val Thr Ser 176	Gln	Arg	Gln	Arg	Glu	Val	Thr	Leu	His	Leu	yeu	Pro	Ile	Ala	Ser	Val	96
His Thr His His Lys Pro Ile Val Phe Leu Leu Asn Ser Pro Gln Pro 112  CTG GTG TGG CAT CTG AAG ACG GAG AGA CTG GCC GCT GGT GTC CCC AGA 384  Leu Val Trp His Leu Lys Thr Glu Arg Leu Ala Ala Gly Val Pro Arg 128  CTC TTC CTG GTT TCG GAG GGT TCT GTG GTC CAG TTT CCA TCA GGA AAC 432  Leu Phe Leu Val Ser Glu Gly Ser Val Val Gln Phe Pro Ser Gly Asn 144  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAT 480  Phe Ser Leu Thr Ala Glu Thr Glu Glu Arg Asn Phe Pro Gln Glu Asn 160  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG 528  Glu His Leu Val Arg Trp Ala Gln Lys Glu Tyr Gly Ala Val Thr Ser 176							3.00	cmc	mm^		CTC	220	ጥርር	ccc	CAG	CCC	336
CTG GTG TGG CAT CTG AAG ACG GAG AGA CTG GCC GCT GGT GTC CCC AGA 384 Leu Val Trp His Leu Lys Thr Glu Arg Leu Ala Ala Gly Val Pro Arg 128  CTC TTC CTG GTT TCG GAG GGT TCT GTG GTC CAG TTT CCA TCA GGA AAC 432 Leu Phe Leu Val Ser Glu Gly Ser Val Val Gln Phe Pro Ser Gly Asn 144  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAT 480 Phe Ser Leu Thr Ala Glu Thr Glu Glu Arg Asn Phe Pro Gln Glu Asn 160  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG 528 Glu His Leu Val Arg Trp Ala Gln Lys Glu Tyr Gly Ala Val Thr Ser 176	CAC	ACT	CAC	CAC	AAA	CCI	TIO	010	Dho	TAN	Len	Agn	Ser	Pro	Gin	Pro	
Leu Val Trp His Leu Lys Thr Glu Arg Leu Ala Ala Gly Val Pro Arg  CTC TTC CTG GTT TCG GAG GGT TCT GTG GTC CAG TTT CCA TCA GGA AAC Leu Phe Leu Val Ser Glu Gly Ser Val Val Gln Phe Pro Ser Gly Asn +  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAT Phe Ser Leu Thr Ala Glu Thr Glu Glu Arg Asn Phe Pro Gln Glu Asn 160  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG Glu His Leu Val Arg Trp Ala Gln Lys Glu Tyr Gly Ala Val Thr Ser  TTC ACT GAA CTC AAG ATA GCA AGA AAC ATC TAT ATT AAA GTG GGA GAA 576	HIB	THE	HIS	uir	гув	PIO	176	Val	1110	200	204		-	•••	<b></b>		
Leu Val Trp His Leu Lys Thr Glu Arg Leu Ala Ala Gly Val Pro Arg  CTC TTC CTG GTT TCG GAG GGT TCT GTG GTC CAG TTT CCA TCA GGA AAC Leu Phe Leu Val Ser Glu Gly Ser Val Val Gln Phe Pro Ser Gly Asn +  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAT Phe Ser Leu Thr Ala Glu Thr Glu Glu Arg Asn Phe Pro Gln Glu Asn 160  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG Glu His Leu Val Arg Trp Ala Gln Lys Glu Tyr Gly Ala Val Thr Ser  TTC ACT GAA CTC AAG ATA GCA AGA AAC ATC TAT ATT AAA GTG GGA GAA 576	CTG	GTG	TGG	CAT	CTG	AAG	ACG	GAG	AGA	CTG	GCC	GCT	GGT	GTC	CCC	AGA	384
CTC TTC CTG GTT TCG GAG GGT TCT GTG GTC CAG TTT CCA TCA GGA AAC Leu Phe Leu Val Ser Glu Gly Ser Val Val Gln Phe Pro Ser Gly Asn + #  TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAT Phe Ser Leu Thr Ala Glu Thr Glu Glu Arg Asn Phe Pro Gln Glu Asn 160 GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG Glu His Leu Val Arg Trp Ala Gln Lys Glu Tyr Gly Ala Val Thr Ser  TTC ACT GAA CTC AAG ATA GCA AGA AAC ATC TAT ATT AAA GTG GGA GAA 576	Leu	Val	Trp	His	Leu	Lys	Thr	Glu	Arg	Leu	Ala	Ala	Gly	Val	Pro	Arg	128
Leu Phe Leu Val Ser Glu Gly Ser Val Val Gln Phe Pro Ser Gly Asn + # # # # # # # # # # # # # # # # # #																	
TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAT 480 Phe Ser Leu Thr Ala Glu Thr Glu Glu Arg Asn Phe Pro Gln Glu Asn 160 GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG 528 Glu His Leu Val Arg Trp Ala Gln Lys Glu Tyr Gly Ala Val Thr Ser 176 TTC ACT GAA CTC AAG ATA GCA AGA AAC ATC TAT ATT AAA GTG GGA GAA 576	CTC	TTC	CTG	GTT	TCG	GAG	GGT	TCT	GTG	GTC	CAG	TTT	CCA	TCA	GGA	AAC	
TTC TCC TTG ACA GCA GAA ACA GAG GAA AGG AAT TTC CCT CAA GAA AAT  480 Phe Ser Leu Thr Ala Glu Thr Glu Glu Arg Asn Phe Pro Gln Glu Asn  160 GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG Glu His Leu Val Arg Trp Ala Gln Lys Glu Tyr Gly Ala Val Thr Ser  TTC ACT GAA CTC AAG ATA GCA AGA AAC ATC TAT ATT AAA GTG GGA GAA  576	Leu	Phe	Leu	Val	Ser	Glu	Gly	Ser	Val	Val	Gln	Phe	Pro	Ser	Gly		144
Phe Ser Leu Thr Ala Glu Thr Glu Glu Arg Asn Phe Pro Gln Glu Asn  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  Glu His Leu Val Arg Trp Ala Gln Lys Glu Tyr Gly Ala Val Thr Ser  TTC ACT GAA CTC AAG ATA GCA AGA AAC ATC TAT ATT AAA GTG GGA GAA  576														+		•	
Phe Ser Leu Thr Ala Glu Thr Glu Glu Arg Asn Phe Pro Gln Glu Asn  GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG  Glu His Leu Val Arg Trp Ala Gln Lys Glu Tyr Gly Ala Val Thr Ser  TTC ACT GAA CTC AAG ATA GCA AGA AAC ATC TAT ATT AAA GTG GGA GAA  576				202	CCN	CDD	ארא	GAG	CAA	<b>A</b> CC	ТАА	TTC	ССТ	CAA	GAA	AAT	480
GAA CAT CTC GTG CGC TGG GCC CAA AAG GAA TAT GGA GCA GTG ACT TCG 528 Glu His Leu Val Arg Trp Ala Gln Lys Glu Tyr Gly Ala Val Thr Ser 176 TTC ACT GAA CTC AAG ATA GCA AGA AAC ATC TAT ATT AAA GTG GGA GAA 576	TTC	TCC	TTG	ACA	Ala ala	GAA	Thr	Glu	Glu	Ara	Asn	Phe	Pro	Gln	Glu	Asn	
Glu His Leu Val Arg Trp Ala Gln Lys Glu Tyr Gly Ala Val Thr Ser 176 TTC ACT GAA CTC AAG ATA GCA AGA AAC ATC TAT ATT AAA GTG GGA GAA 576	rne	ber	Den	* 117	ard		- ***										
Glu His Leu Val Arg Trp Ala Gln Lys Glu Tyr Gly Ala Val Thr Ser 176 TTC ACT GAA CTC AAG ATA GCA AGA AAC ATC TAT ATT AAA GTG GGA GAA 576	GAA	САТ	CTC	GTG	CGC	TGG	GCC	CAA	λAG	GAA	TAT	GGA	GCA	GTG	ACT	TCG	528
TTC ACT GAA CTC AAG ATA GCA AGA AAC ATC TAT ATT AAA GTG GGA GAA 576	Glu	His	Leu	Val	Arg	Trp	Ala	Gln	Lys	Glu	Tyr	Gly	Ala	Val	Thr	Ser	176
TTC ACT GAA CTC AAG ATA GCA AGA AAC ATC TAT ATT AAA GTG GGA GAA 576																	
	TTC	ACT	GAA	CTC	AAG	ATA	GCA	AGA	AAC	ATC	TAT	ATT	AAA	GTG	GGA	GAA	
Phe Thr Glu Leu Lys Ile Ala Arg Asn Ile Tyr Ile Lys Val Gly Glu 192	Phe	Thr	Glu	Leu	Lys	Ile	Ala	Arg	Asn	Ile	Tyr	Ile	Lys	Val	Gly	Glu	192

2/7

#### FIGURE 1B

																	<b>CO</b> 4
													TAA				624
	Asp	Gln	Val	Phe	Pro	Pro	Thr	Сув	Asn	Ile	Gly	Lys	Asn	Phe	Leu	Ser	208
								£									•
			<b></b>	~~~		C > C	ma c	СФФ	CAA	CCC	222	GCC	GCC	CAA	сст	TGT	672
	CTC	AAT	TAC	CIT	310	Clu	TNC	Tou	Gla	Pro	Tue	Ala	Ala	Glu	Glv	Cvs	224
	Leu	ABN	TYE	Leu	Ala	GIU	ıyı	Leu	QIII	FIO	Lye	n.u		014	011	- Ç	
																_	
	GTC	CTG	CCC	AGT	CAG	ccc	CAT	GAA	AAG	GAA	GTA	CAC	ATC	ATC	GAG	TTA	720
													Ile				240
	ATT	ACC	CCC	AGC	TCG	AAC	CCT	TAC	AGC	GCT	TTC	CAG	GTG	GAT	ATA	ATA	768
	Ile	Thr.	Pro	Ser	Ser	Asn	Pro	Tyr	Ser	Ala	Phe	Gln	Val	Asp	Ile	Ile	256
							<b></b>	~~~	<b>~~</b>		C2C	CTC	CTC		NAC.	C-Tr-Tr	816
	GTT	GAC	ATA	CGA	CCT	GCT	CAA	GAG	GAT	Dec	CAG	010	GTC	tue	Anc	Tou	272
	Val	Asp	He	Arg	Pro	AIA	GIN	GIU	Авр	PIO	GIU	Val	Val	Lyb	VDII	Dea	2,2
	GTC	CTG	ATC	TTG	AAG	TGC	AAA	AAG	TCT	GTC	AAC	TGG	GTG	ATC	AAG	TCT	864
													Val				288
					-	•	-										
																	010
	TTT.	GAC	GTC	AAG	GGA	AAC	TTG	AAA	GTC	ATT	GCT	CCC	AAC	AGT	ATC	GGC	912
	Phe	увь	Val	Lys	Gly	Asn	Leu	Lys	Val	He	YIG	Pro	Asn	ser	He	GIĀ	304
	արդու	CCA	222	GAG	AGT	GAA	CGA	TCC	ATG	ACA	ATG	ACC	AAA	TTG	GTA	AGA	960
	Phe	Glv	Lvs	Glu	Ser	Glu	Ara	Ser	Met	Thr	Met	Thr	Lys	Leu	Val	λrg	320
		_	_														
													TGG				1008
	Авр	Авр	Ile	Pro	Ser	Thr	Gln	Glu	Asn	Leu	Met	Lys	Trp	Ala	Leu	Asp	336
																	1056
	AAT	GGC	TAC	AGG	CCA	GTG	ACG	TCA	TAC	ACA	ATG	GCT	CCC	GTG	GCT	AAT	1056 352
	Asn	Gly	Tyr	Arg	Pro	Val	Thr	ser	Tyr	Thr	Met	ATS	Pro	vai	AIA	ABD	352
	ACA	ጥጥጥ	СУТ	CTT	CCG	CTT	GAG	AAC	AAC	GAG	GAG	ATG	AGA	GAT	GAG	GAA	1104
																	368
	_				3								_	_			
•	GTC	CAC	ACC	ATT	CCT	CCT	GAG	CTT	CGT	ATC	CTG	CTG	GAC	CCT	GAC	CAC	1152
													Авр				384
		,	•								P	epti	de 1				
													CC3	300	CCN	330	1200
	CCG	CCC	GCC	CTG	GAC	AAC	CCA	CTC	TTC	CCA	Clas	CAG	GGA	SOT	Dro	vui	400
	Pro	Pro	Ala	ren	Asp	ABN	PTO	Ten	rne	PFO	erà	GIU	GJÀ	ser	FIO	Vali	400
	GGT	CCT	СТС	ccc	TTT	CCA	TTC	CCG	GAT	ATC	CCC	AGG	AGA	GGC	TGG	AAG	1248
•	Clu	Glv	Len	Pro	Phe	Pro	Phe	Pro	Asp	Ile	Pro	Arg	Arg	Gly	Trp	Lys	416
	_	_															
	GAG	GGC	GAA	GAT	AGG	ATC	CCC	CGG	CCA	AAG	CAG	CCC	ATC	GTT	CCC	AGT	1296
	Glu	G1y	Glu	Asp	Arg	Ile	Pro	Arg	Pro	Lys	Gln	Pro	Ile	Val	Pro	Ser	432
	•	•		_									tide				

3/7

## FIGURE 1C

CTT																
	CAA	CTG	CTT	CCT	GAC	CAC	CGA	GAA	CCA	GAA	GAA	GTG	CAA	GGG	GGC	1344
														Gly		448
VAI	GIN	rea	rea	Pro	ивр	UIB	ALY	GIU	PLO	GIU	GIU	Val	<b>U</b> 111	O1,	01,	
GTG	GAC	ATC	GCC	CTG	TCA	GTC	AAA	TGT	GAC	CAT	GAA	AAG	ATG	GTC	GTG	1392
														Val		464
AGI	Mab	116	VIG	Leu	Ser	101	270	_				_,_				
								£								
CCT	CTA	CAC	AAA	GAC	TCT	TTC	CAG	ACC	AAT	GGC	TAC	TCA	GGG	ATG	GAG	1440
														Met		480
Ala	vai	Asp	ГÀВ	Авр	ser	Phe	GIII	1111	VBII	GIA	TAT	SEL	Gry	Mec	<b>G1</b>	100
												+				
CTC	ACC	CTG	TTG	GAT	CCT	TCG	TGT	AAA	GCC	AAA	ATG	AAT	GGT	ACT	CYC	1488
														Thr		496
rea	THE	reu	reu	veb	PIO	SEL	_	בענם	NI.	LJB	1100	_	<b>U</b> -,			
							£					#				
TTT	GTT	CTC	GAG	TCT	CCC	CTG	AAT	GGC	TGT	GGT	ACT	CGA	CAT	CGG	AGG	1536
														Arg		512
FIIE	AGI	Dea	GIU	Jei	110	204	*****	,	_	,		9		9	3	
									&							
TCG	ACC	CCG	GAT	GGT	GTG	GTT	TAC	TAT	AAC	TCT	ATT	GTG	GTG	CAG	<b>GCT</b>	1584
														Gln		528
				,			-1-	-3-					_			
																1622
														GAC		1632
Pro	Ser	Pro	Gly	Asp	Ser	Ser	Gly	Trp	Pro	Asp	Gly	Tyr	Glu	Asp	Leu	544
						+++										
•						+++										
	. • •							663	<b>63.0</b>	666	CNT	CAA	CCA	CAA	» Corr	1680
						TTT								GAA		1680
						TTT								GAA Glu		1680 560
						TTT										
	Ser					TTT										
Glu	Ser +	Gly	Asp	Asn	Gly	TTT Phe	Pro	Gly	Авр	Gly	Asp	Glu	Gly	Glu	Thr	560
Glu . GCC	Ser + CCC	CTG	AGC	Asn	Gly GCT	TTT Phe GGA	Pro GTG	Gly GTG	Asp	Gly	ABP	Glu TGC	Gly AGC	Glu TTG	Thr	1728
Glu . GCC	Ser + CCC	CTG	AGC	Asn	Gly GCT	TTT Phe GGA	Pro GTG	Gly GTG	Asp	Gly	ABP	Glu TGC	Gly AGC	Glu	Thr	560
Glu . GCC	Ser + CCC	CTG	AGC	Asn	Gly GCT	TTT Phe GGA	Pro GTG	Gly GTG	Asp	Gly	ABP	Glu TGC	Gly AGC	Glu TTG	Thr	1728
Glu . GCC	Ser + CCC	CTG	AGC	Asn	Gly GCT	TTT Phe GGA	Pro GTG	Gly GTG	Asp	Gly	AAC Aan	Glu TGC Cys	Gly AGC	Glu TTG	Thr	1728
GCC Ala	Ser + CCC Pro	CTG Leu	Asp AGC Ser	Asn CGA Arg	Gly GCT Ala	TTT Phe GGA Gly	Pro GTG Val	GTG Val	Asp GTG Val	Gly TTT Phe	ABP AAC ABN	Glu TGC Cys	Gly AGC Ser	Glu TTG Leu	Thr CGG Arg	1728 576
GCC Ala	Ser + CCC Pro	Gly CTG Leu AGG	Asp AGC Ser	Asn CGA Arg	Gly GCT Ala AGT	TTT Phe GGA Gly	Pro GTG Val	Gly GTG Val	Asp GTG Val	Gly TTT Phe	ABP  AAC ABn  #  CTC	Glu TGC Cys & GAT	Gly AGC Ser	Glu TTG Leu AAT	Thr CGG Arg	1728 576
GCC Ala	Ser + CCC Pro	Gly CTG Leu AGG	Asp AGC Ser	Asn CGA Arg	Gly GCT Ala AGT	TTT Phe GGA Gly	Pro GTG Val	Gly GTG Val	Asp GTG Val	Gly TTT Phe	ABP  AAC ABn  #  CTC	Glu TGC Cys & GAT	Gly AGC Ser	Glu TTG Leu	Thr CGG Arg	1728 576
GCC Ala	Ser + CCC Pro	Gly CTG Leu AGG	Asp AGC Ser	Asn CGA Arg	Gly GCT Ala AGT	TTT Phe GGA Gly	Pro GTG Val	Gly GTG Val	Asp GTG Val	Gly TTT Phe	ABP  AAC ABn  #  CTC	Glu TGC Cys & GAT	Gly AGC Ser	Glu TTG Leu AAT	Thr CGG Arg	1728 576
GCC Ala	Ser + CCC Pro	Gly CTG Leu AGG	Asp AGC Ser	Asn CGA Arg	Gly GCT Ala AGT	TTT Phe GGA Gly	Pro GTG Val	Gly GTG Val	Asp GTG Val	Gly TTT Phe	ABP  AAC ABn  #  CTC	Glu TGC Cys & GAT	Gly AGC Ser	Glu TTG Leu AAT	Thr CGG Arg	1728 576
GCC Ala CAG Gln	Ser + CCC Pro CTG Leu	CTG Leu AGG Arg	AGC Ser AAT ABn	CGA Arg CCC Pro	Gly GCT Ala AGT Ser	TTT Phe GGA Gly GGC Gly	GTG Val TTC Phe	Gly GTG Val CAG Gln	GTG Val GGC Gly	Gly TTT Phe CAG Gln	ABP  AAC Asn  CTC Leu	TGC Cys & GAT Asp	AGC Ser GGA Gly	Glu TTG Leu AAT Asn	CGG Arg GCT Ala	1728 576 1776 592
GCC Ala CAG Gln	Ser + CCC Pro CTG Leu	CTG Leu AGG Arg	AGC Ser AAT ABN	Asn CGA Arg CCC Pro	Gly GCT Ala AGT Ser	TTT Phe GGA Gly GGC Gly	GTG Val TTC Phe	Gly GTG Val CAG Gln	GTG Val GGC Gly	Gly TTT Phe CAG Gln CTC	ABP  AAC ABn  #  CTC Leu  TTT	TGC Cys & GAT Asp	AGC Ser GGA Gly	TTG Leu AAT ABN	Thr CGG Arg GCT Ala	1728 576 1776 592
GCC Ala CAG Gln	Ser + CCC Pro CTG Leu	CTG Leu AGG Arg	AGC Ser AAT ABN	Asn CGA Arg CCC Pro	Gly GCT Ala AGT Ser	TTT Phe GGA Gly GGC Gly	GTG Val TTC Phe	Gly GTG Val CAG Gln	GTG Val GGC Gly	Gly TTT Phe CAG Gln CTC	ABP  AAC ABn  #  CTC Leu  TTT	TGC Cys & GAT Asp	AGC Ser GGA Gly	Glu TTG Leu AAT Asn	Thr CGG Arg GCT Ala	1728 576 1776 592
GCC Ala CAG Gln ACC	Ser + CCC Pro CTG Leu TTC	CTG Leu AGG Arg AAC	ABP AGC Ser AAT ABn ATG Met	CGA Arg CCC Pro GAG Glu	Gly GCT Ala AGT Ser CTG Leu	TTT Phe GGA Gly GGC Gly	GTG Val TTC Phe AAC Asn	Gly GTG Val CAG Gln ACA Thr	GTG Val GGC Gly GAC ABP	Gly TTT Phe CAG Gln CTC Leu	ASP  AAC Asn  #  CTC Leu  TTT Phe	TGC Cys & GAT Asp CTG Leu	Gly AGC Ser GGA Gly GTG Val	TTG Leu AAT Asn #	Thr CGG Arg GCT Ala TCC Ser	1728 576 1776 592 1824 608
GCC Ala CAG Gln ACC	Ser + CCC Pro CTG Leu TTC	CTG Leu AGG Arg AAC	ABP AGC Ser AAT ABn ATG Met	CGA Arg CCC Pro GAG Glu	Gly GCT Ala AGT Ser CTG Leu	TTT Phe GGA Gly GGC Gly	GTG Val TTC Phe AAC Asn	Gly GTG Val CAG Gln ACA Thr	GTG Val GGC Gly GAC ABP	Gly TTT Phe CAG Gln CTC Leu	ASP  AAC Asn  #  CTC Leu  TTT Phe	TGC Cys & GAT Asp CTG Leu	Gly AGC Ser GGA Gly GTG Val	TTG Leu AAT Asn #	Thr CGG Arg GCT Ala TCC Ser	1728 576 1776 592
Glu GCC Ala CAG Gln ACC Thr	Ser + CCC Pro CTG Leu TTC Phe	CTG Leu AGG Arg AAC ABn	ABP AGC Ser AAT ABn ATG Met	Asn CGA Arg CCC Pro GAG Glu TCT	Gly GCT Ala AGT Ser CTG Leu GTG	TTT Phe GGA Gly GGC Gly TAT Tyr	GTG Val TTC Phe AAC Asn	GTG Val CAG Gln ACA Thr	GTG Val GGC Gly GAC ABP	Gly TTT Phe CAG Gln CTC Leu CAT	Asp AAC Asn  f CTC Leu TTT Phe GTT	TGC Cys & GAT Asp CTG Leu	Gly AGC Ser GGA Gly GTG Val	TTG Leu AAT Asn # CCC Pro	Thr CGG Arg GCT Ala TCC Ser GTG	1728 576 1776 592 1824 608
Glu GCC Ala CAG Gln ACC Thr	Ser + CCC Pro CTG Leu TTC Phe	CTG Leu AGG Arg AAC ABn	ABP AGC Ser AAT ABn ATG Met	Asn CGA Arg CCC Pro GAG Glu TCT	Gly GCT Ala AGT Ser CTG Leu GTG	TTT Phe GGA Gly GGC Gly TAT Tyr	GTG Val TTC Phe AAC Asn	GTG Val CAG Gln ACA Thr	GTG Val GGC Gly GAC ABP	Gly TTT Phe CAG Gln CTC Leu CAT	Asp AAC Asn  f CTC Leu TTT Phe GTT	TGC Cys & GAT Asp CTG Leu	Gly AGC Ser GGA Gly GTG Val	TTG Leu AAT Asn #	Thr CGG Arg GCT Ala TCC Ser GTG	1728 576 1776 592 1824 608
GCC Ala CAG Gln ACC Thr	Ser + CCC Pro CTG Leu TTC Phe GGG Gly	CTG Leu AGG Arg AAC Asn GTC	ASP AGC SET AAT ABN ATG Met TTC Phe	CGA Arg CCC Pro GAG Glu TCT Ser	Gly GCT Ala AGT Ser CTG Leu GTG Val	TTT Phe GGA Gly GGC Gly TAT Tyr GCA Ala	GTG Val TTC Phe AAC Asn GAG Glu	GTG Val CAG Gln ACA Thr	GTG Val GGC Gly GAC Asp GAG Glu	Gly TTT Phe CAG Gln CTC Leu CAT His	Asp AAC Asn  f CTC Leu TTT Phe GTT Val	TGC Cys & GAT Asp CTG Leu TAT	Gly AGC Ser GGA Gly GTG Val	TTG Leu AAT Asn # CCC Pro GAG Glu	CGG Arg GCT Ala TCC Ser GTG Val	1728 576 1776 592 1824 608 1872 624
GCC Ala CAG Gln ACC Thr CCA Pro	Ser + CCC Pro CTG Leu TTC Phe GGG Gly	CTG Leu AGG Arg AAC ABn GTC Val	AGC Ser AAT ABN Met TTC Phe AAG	Asn CGA Arg CCC Pro GAG Glu TCT Ser GCT	Gly GCT Ala AGT Ser CTG Leu GTG Val	TTT Phe GGA Gly GGC Gly TAT Tyr GCA Ala	GTG Val TTC Phe AAC ABN GAG Glu	Gly GTG Val CAG Gln ACA Thr AAC ASn	GTG Val GGC Gly GAC ABP GAG Glu	Gly TTT Phe CAG Gln CTC Leu CAT His	Asp AAC Asn  CTC Leu TTT Phe GTT Val	TGC Cys & GAT Asp CTG Leu TAT Tyr	Gly AGC Ser GGA Gly GTG Val GTT Val	TTG Leu AAT Asn # CCC Pro GAG Glu ACC	Thr  CGG Arg  GCT Ala  TCC Ser  GTG Val  TGC	1728 576 1776 592 1824 608 1872 624
GCC Ala CAG Gln ACC Thr CCA Pro	Ser + CCC Pro CTG Leu TTC Phe GGG Gly	CTG Leu AGG Arg AAC ABn GTC Val	AGC Ser AAT ABN Met TTC Phe AAG	Asn CGA Arg CCC Pro GAG Glu TCT Ser GCT	Gly GCT Ala AGT Ser CTG Leu GTG Val	TTT Phe GGA Gly GGC Gly TAT Tyr GCA Ala	GTG Val TTC Phe AAC ABN GAG Glu	Gly GTG Val CAG Gln ACA Thr AAC ASn	GTG Val GGC Gly GAC ABP GAG Glu	Gly TTT Phe CAG Gln CTC Leu CAT His	Asp AAC Asn  CTC Leu TTT Phe GTT Val	TGC Cys & GAT Asp CTG Leu TAT Tyr	Gly AGC Ser GGA Gly GTG Val GTT Val	TTG Leu AAT Asn # CCC Pro GAG Glu	Thr  CGG Arg  GCT Ala  TCC Ser  GTG Val  TGC	1728 576 1776 592 1824 608 1872 624

4/7

#### FIGURE 1D

TTT	CTC	TCT	CCA	TAC	TCC	AAC	CCA	GAC	AGA	ATG	TCT	GAT	TAC	ACC	ATC	1968
Phe	T.em	Ser	Pro	Tvr	Ser	Agn	Pro	ABD	Arg	Met	Ser	Asp	Tyr	Thr	Ile	6 <del>5</del> 6
2 110	200			-1-					5			•	-			
										cmc	220	mme	TAC	300	TCC	2016
ATC	GAG	AAC	ATC	TGT	CCG	AAA	GAC	GAC	TCT	GIG	MAG	110	INC	AGC	100	
Ile	Glu	Asn	Ile	Сув	Pro	Lys	Asp	Asp	Ser	Val	Lys	Pne	Tyr	Ser	Ser	672
				&												
AAG	PCP	GTG	CAC	ጥጥጥ	CCC	ATC	CCG	CAT	GCT	GAG	GTG	GAC	AAG	AAG	CGC	2064
Tara	Non	V-1	Wi.c.	Pho	200	710	Dro	uio	Ala	Glu	Val	Ago	T.VB	Lys	Ara	688
гав	Arg	ANT	UIB	FIIE	PIU	116	PIO	HIL	nza	014	***		-,-	-,-		
															~~~	2112
TTC	AGC	TTC	CTG	TTC	AAG	TCT	GTG	TTC	AAC	ACC	TCC	CIG	CIC	TTC	CIG	
Phe	Ser	Phe	Leu	Phe	Lys	Ser	Val	Phe	Asn	Thr	Ser	Leu	Leu	Phe	Leu	704
•									#							
													•			
030	mcc	CNC	<b>PPC</b>	в сет	CTC.	TGC	TCC	AGG	DAG	DAG	GGC	TCC	CTG	AAG	CTG	2160
CAC	160	GAG	110	MCI	T	200	500	7-0	7	T >= 0	Glw	Sor	Lev	T.vo	Leu	720
H1B	Cys	GIU	rea	Thr	rea		ser	Arg	rys	rys	Gly	Ser	200	Lys	200	,,,
	£					&										•
CCG	AGG	TGT	GTG	ACT	CCT	GAC	GAC	GCC	TGC	ACT	TCT	CTC	GAT	GCC	ACC	2208
Pro	Ara	Cvs	Val	Thr	Pro	αaA	Asp	Ala	Сув	Thr	Ser	Leu	Авр	Ala	Thr	736
	5	3					•		۔		•		_			
		•							_							
										202	mmo	200	220	000	CTC	2256
ATG	ATC	TGG	ACC	ATG	ATG	CAG	AAT	AAG	AAG	ACA	TIC	ACC	AAG	CCC		752
Met	Ile	Trp	Thr	Met	Met	Gln	Asn	Lys	Lys	Thr	Pne	Thr	гав	Pro	Pen	/52
GCT	GTG	GTC	CTC	CAG	GTA	GAC	TAT	AAA	GAA	AAT	GTT	CCC	AGC	ACT	AAG	2304
Ala	Val	Val	Leu	Gln	Val	Asp	Tvr	Lvs	Glu	Asn	Val	Pro	Ser	Thr	Lys	768
								•							_	
~~m	maa	300	003	አጥጥ	COTT	CCT	CCT	ССТ	CCA	CAG	<b>ል</b> ሞሞ	TTC	CAT	GGC	CTG	2352
GAT	TCC	WGI	CUA	MII		201	5	5	2	C1-	710	Bho	ui.	Clv	Lou	784
Asp	Ser	Ser	Pro	He	Pro	PTO	Pro	Pro	PIO	GIII	116	File	UIB	Gly	Leu	,04
	•															
GAC	ACG	CTC	ACC	GTG	ATG	GGC	ATT	GCA	TTT	GCA	GCA	TTT	GTG	ATC	GGA	2400
Asp	Thr	Leu	Thr	Val	Met	Gly	Ile	Ala	Phe	Ala	Ala	Phe	Val	Ile	Gly	800
ccc	CTC	CTC	ACG	ccc	GCC	TTG	TGG	TAC	ATC	TAC	TCC	CAC	ACA	GGG	GAG	2448
33.			Wr-	63	33-	T 011	T	Mar	710	Tur	Sor	Hie	Thr	Gly	Glu	816
Ala	Leu	Leu	Thr	GIY	WIG	<u> Leu</u>	TIP	171	116	777	<u> </u>	HID	****	013	014	
																2406
ACA	GCA	CGA	AGG	CAG	CAA	GTC	CCT	ACC	TCG	CCG	CCA	GCC	TCG	GAG	AAC	2496
Thr	Ala	Arq	Arq	Gln	Gln	Val	Pro	Thr	Ser	Pro	Pro	Ala	Ser	Glu	Asn	832
S	9	•	•													
•	_															
300			~~~	CAC	300	D.T.C	cec	<b>VCC</b>	እርጥ	CAG	ACT	ACC	CCC	TGC	TCT	2544
AGC	AGC	فاتان	900	CAC	AGC	VIC.	00C	Com	WP-	C1-		Th-	D-^	Circ	50-	848
Ser	Ser	Ala	Ala	His	ser	TIE	GIY	ser	inr	GIN	ser	Int	FIO	Cys	SEL	040
AGC	AGC	AGC	ACA	GCC	TAG	GTGG:	ACA (	GACA	GACG	cc c	GCCC	ACCG	C AG	CCAG	GGCA	2599
				Ala												853

PCT/US92/09326

#### 5/7

#### FIGURE 1E

GGGCCCGATG	CCAGTGCTGC	GTGTCCACAG	TCAGAAGTCT	TGATCTGGGC	TCCCTGTAAA	2659
GAAAGAGTGA	ATTTCAGTAT	ACAGACAGCC	AGTTCTACCC	ACCCCTTACC	ACGGCCCACA	2719
TAAATGTGAC	CCTGGGCATC	TGTCACACGA	AAGCTAAGCT	GGTGGCCTTC	CCCACCAGCC	2779
CCTCCCAGGA	TEGGGGTTTC	AATGTGAAAC	ATCTGCCAGT	TTTGTTTTGT	TTTTTTAATG	2839
CTCCTTTCTC	CAGGTGTCCA	AACATCCATC	ATTTGGGGTG	GTCTGTTTTA	CAGAGTAAAG	2899
CACCCCCCA	AGGGACGTCA	GCTAGTGTGT	AGAGCCAAGG	GGAGACAGCT	AGGATTCTCG	2959
		AAATAGAAGA				2997

PCT/US92/09326

6/7

### FIGURE 2

				GTTGGCGAGG
AGTTTCCTGT	TTCCCCCGCA	GCGCTGAGTT	GAAGTTGAGT	GAGTCACTCG
CGCGCACGGA	GCGACGACAC	CCCCGCGCGT	GCACCCGCTC	GGGACAGGAG
CCGGACTCCT	GTGCAGCTTC	CCTCGGCCGC	CGGGGGCCTC	CCCGCGCCTC
GCCGGCCTCC	AGGCCCCTCC	TGGCTGGCGA	GCGGGCGCCA	CATCTGGCCC
GCACATCTGC	GCTGCCGGCC	CGGCGCGGG	TCCGGAGAGG	GCGCGGCGCG
GAGCGCAGCC	AGGGGTCCGG	GAAGGCGCCG	TCCGTGCGCT	GGGGGCTCGG
TCTATGACGA	GCAGCGGGGT	CTGCCATGGG	TCGGGGGCTG	CTCAGGGGCC
TGTGGCCGCT	GCACATCGTC	CTGTGGACGC	GTATCGCCAG	CACGATCCCA
CCGCACGTTC	AGAAGTCGGT	TAATAACGAC	ATGATAGTCA	CTGACAACAA
CGGTGCAGTC	AAGTTTCCAC	AACTGTGTAA	attttgtgat	GTGAGATTTT
CCACCTGTGA	CAACCAGAAA	TCCTGCATGA	GCAACTGCAG	CATCACCTCC
ATCTGTGAGA	AGCCACAGGA	agtctgtgtg	GCTGTATGGA	GAAAGAATGA
CGAGAACATA	<b>ACACTAGAGA</b>	CAGTTTGCCA	TGACCCCAAG	CTCCCCTACC
ATGACTTTAT	TCTGGAAGAT	GCTGCTTCTC	Caragicat	TATGAAGGAA
AAAAAAAAGC	CTGGTGAGAC	TTTCTTCATG	TGTTCCTGTA	GCTCTGATGA
GTGCAATGAC	<b>AACATCATCT</b>	TCTCAGAAGA	ATATAACACC	AGCAATCCTG
ACTTGTTGCT	AGTCATATTT	CAAGTGACAG	GCATCAGCCT	CCTGCCACCA
CTGGGAGTTG	CCATATCTGT	CATCATCATC	TTCTACTGCT	ACCGCGTTAA
CCGGCAGCAG	<b>AAGCTGAGTT</b>	CAACCTGGGA	AACCGGCAAG	ACGCGGAAGC
TCATGGAGTT	CAGCGAGCAC	TGTGCCATCA	TCCTGGAAGA	TGACCGCTCT
GACATCAGCT	CCACGTGTGC	CAACAACATC	AACCACAACA	CAGAGCTGCT
GCCCATTGAG	CTGGACACCC	TGGTGGGGAA	AGGTCGCTTT	GCTGAGGTCT
ATAAGGCCAA	GCTGAAGCAG	AACACTTCAG	AGCAGTTTGA	GACAGTGGCA
GTCAAGATCT	TTCCCTATGA	GGAGTATGCC	TCTTGGAAGA	CAGAGAAGGA
CATCTTCTCA	GACATCAATC	TGAAGCATGA	GAACATACTC	CAGTTCCTGA
CGGCTGAGGA	GCGGAAGACG	GAGTTGGGGA	AACAATACTG	GCTGATCACC
GCCTTCCACG	CCAAGGGCAA	CCTACAGGAG	TACCTGACGC	GGCATGTCAT
CAGCTGGGAG	GACCTGCGCA	AGCTGGGCAG	CTCCCTCGCC	CGGGGGATTG
CTCACCTCCA	CAGTGATCAC	ACTCCATGTG	GGAGGCCCAA	GATGCCCATC
GTGCACAGGG	ACCTCAAGAG	CTCCAATATC	CTCGTGAAGA	ACGACCTAAC
CTGCTGCCTG	TGTGACTTTG	GGCTTTCCCT	GCGTCTGGAC	CCTACTCTGT
CTGTGGATGA	CCTGGCTAAC	AGTGGGCAGG	TGGGAACTGC	AAGATACATG
GCTCCAGAAG	TCCTAGAATC	CAGGATGAAT	TTGGAGAATG	CTGAGTCCTT
CAAGCAGACC	GATGTCTACT	CCATGGCTCT	GGTGCTCTGG	GAAATGACAT
CTCGCTGTAA	TGCAGTGGGA	GAAGTAAAAG	ATTATGAGCC	TCCATTTGGT
TCCAAGGTGC	GGGAGCACCC	CTGTGTCGAA	AGCATGAAGG	ACAACGTGTT
GAGAGATCGA	GGGCGACCAG	AAATTCCCAG	CTTCTGGCTC	AACCACCAGG
GCATCCAGAT	GGTGTGTGAG	ACGTTGACTG	AGTGCTGGGA	CCACGACCCA
GAGGCCCGTC	TCACAGCCCA	GTGTGTGGCA	GAACGCTTCA	GTGAGCTGGA
GCATCTGGAC	AGGCTCTCGG	GGAGGAGCTG	CTCGGAGGAG	AAGATTCCTG
AAGACGGCTC	CCTAAACACT	ACCAAATAGC	TCTTATGGGG	CAGGCTGGGC
ATGTCCAAAG	AGGCTGCCCC	TCTCACCAAA		

7/7

#### FIGURE 3

MGRGLLRGLW	PLHIVLWTRI	ASTIPPHVQK	SVNNDMIVTD	NNGAVKPPQL
CKFCDVRFST	CDNQKSCMSN	CSITSICEKP	<b>QEVCVAVWRK</b>	NDENITLETV
CHDPKLPYHD	FILEDAASPK	CIMKEKKKPG	ETFFMCSCSS	DECNDNIIFS
EEYNTSNPDL	LLVIPOVTGI	SLLPPLGVAI	SVIIIFYCYR	VNRQQKLSST
WETGKTRKLM	EFSEHCAIIL	EDDRSDISST	CANNINHNTE	LLPIELDTLV
GKGRFAEVYK	AKLKONTSEQ	FETVAVKIFP	YEEYASWKTE	KDIFSDINLK
HENILOFLTA	EERKTELGKO	YWLITAFHAK	GNLQEYLTRH	VISWEDLRKL
GSSLARGIAH	LHSDHTPCGR	PKMPIVHRDL	KSSNILVKND	LTCCLCDFGL
SLRLDPTLSV	DDLANSGQVG	TARYMAPEVL	ESRMNLENAE	SFKOTDVYSM
ALVLWENTSR	CNAVGEVKDY	EPPFGSKVRE	HPCVESMKDN	VLRDRGRPEI
PSFWLNHQGI	OMVCETLTEC	WDHDPEARLT	AOCVAERFSE	LEHLDRLSGR
SCSEEKIPED	GSLNTTK			
SCSPOVILDA	GOTHIIK			

International Application No

L CLASSIFICATION OF SUBJ	ECT MATTER (if several classification symb	ols apply, indicate all) <sup>6</sup>								
	Classification (IPC) or to both National Class C12N5/10;	ification and IPC	C07K13/00							
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	Documentation Searched other that to the Extent that such Documents are	n Minimum Documentation Included in the Fields Searched <sup>8</sup>	•							
	I. DOCUMENTS CONSIDERED TO BE RELEVANT <sup>9</sup> Attempty <sup>a</sup> Citation of Document, <sup>11</sup> with indication, where appropriate, of the relevant passages <sup>12</sup> Relevant to Claim No. <sup>13</sup>									
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